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(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS

(57) Abstract: The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, ex-
pression vectors for these DNAs, transformed eukaryotic cells expressing these DNAs and antibodies directed to these proteins.

DESCRIPTION

Human Proteins Having Hydrophobic
Domains and DNAs Encoding These Proteins

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TECHNICAL FIELD

The present invention relates to human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, eukaryotic cells expressing these DNAs and antibodies directed to these proteins. The proteins of the present invention can be employed as pharmaceuticals or as antigens for preparing antibodies directed to these proteins. The human cDNAs of the present invention can be utilized as probes for genetic diagnosis and gene sources for gene therapy. Furthermore, the cDNAs can be utilized as gene sources for producing the proteins encoded by these cDNAs in large quantities. Cells into which these genes are introduced to express secretory proteins or membrane proteins in large quantities can be utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like. The antibodies of the present invention can be utilized for the detection, quantification, purification and the like of the proteins of the present invention.

25

BACKGROUND ART

Cells secrete many proteins extracellularly. These secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport, the biophylaxis, and the like of the cells. Unlike intracellular proteins, the secretory proteins exert their actions outside the cells. Therefore, they can be administered in the intracorporeal manner such as the injection or the drip, so that they possess hidden potentialities as pharmaceuticals. In fact, a number of human secretory proteins such as interferons, interleukins, erythropoietin, thrombolytic agents and the like are currently employed as pharmaceuticals. In addition, secretory proteins other than those described above are undergoing clinical trials for developing their use as pharmaceuticals. It is believed that the human cells produce many unknown secretory proteins. Availability of these secretory proteins as well as genes encoding them is expected to lead to development of novel pharmaceuticals utilizing them.

On the other hand, membrane proteins play important roles, as signal receptors, ion channels, transporters and the like in the material transport and the signal transduction through the cell membrane. Examples thereof include receptors for various cytokines, ion

channels for the sodium ion, the potassium ion, the chloride ion and the like, transporters for saccharides and amino acids and the like. The genes for many of them have already been cloned. It has been clarified that abnormalities in these membrane proteins are involved in a number of previously cryptogenic diseases. Therefore, discovery of a new membrane protein is expected to lead to elucidation of the causes of many diseases, so that isolation of new genes encoding the membrane proteins has been desired.

Heretofore, due to difficulty in the purification from human cells, many of these secretory proteins and membrane proteins have been isolated by genetic approaches. A general method is the so-called expression cloning method, in which a cDNA library is introduced into eukaryotic cells to express cDNAs, and the cells secreting, or expressing on the surface of membrane, the protein having the activity of interest are then screened. However, only genes for proteins with known functions can be cloned by using this method.

In general, a secretory protein or a membrane protein possesses at least one hydrophobic domain within the protein. After synthesis on ribosomes, such domain works as a secretory signal or remains in the phospholipid membrane to be entrapped in the membrane. Accordingly, if the existence of a highly hydrophobic domain is observed in the amino acid sequence of a protein encoded by a cDNA when the

whole base sequence of the full-length cDNA is determined, it is considered that the cDNA encodes a secretory protein or a membrane protein.

5 OBJECTS OF INVENTION

The main object of the present invention is to provide novel human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, transformed eukaryotic cells that are capable of
10 expressing these DNAs and antibodies directed to these proteins. This object as well as other objects and advantages of the present invention will become apparent to those skilled in the art from the following description with reference to the accompanying drawings.

15

SUMMARY OF INVENTION

As the result of intensive studies, the present inventors have successfully cloned cDNAs encoding proteins having hydrophobic domains from the human full-length cDNA
20 bank, thereby completing the present invention. Thus, the present invention provides a human protein having hydrophobic domain(s), namely a protein comprising any one of an amino acid sequence selected from the group consisting of SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and
25 121 to 130. Moreover, the present invention provides a DNA

encoding said protein, exemplified by a cDNA comprising any one of a base sequence selected from the group consisting of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150, an expression vector that is capable of expressing
5 said DNA by in vitro translation or in eukaryotic cells, a transformed eukaryotic cell that is capable of expressing said DNA and of producing said protein and an antibody directed to said protein.

10 BRIEF DESCRIPTION OF DRAWINGS

Fig. 1 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03171.

Fig. 2 illustrates the
15 hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03424.

Fig. 3 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03444.

20 Fig. 4 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03478.

Fig. 5 illustrates the
25 hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03499.

Fig. 6 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03500.

Fig. 7 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10691.

Fig. 8 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10703.

Fig. 9 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10711.

Fig. 10 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10712.

Fig. 11 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03010.

Fig. 12 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03576.

Fig. 13 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03611.

Fig. 14 illustrates the

hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03612.

Fig. 15 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
5 by clone HP10407.

Fig. 16 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10713.

Fig. 17 illustrates the
10 hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10714.

Fig. 18 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10716.

Fig. 19 illustrates the
15 hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10717.

Fig. 20 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
20 by clone HP10718.

Fig. 21 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03745.

Fig. 22 illustrates the
25 hydrophobicity/hydrophilicity profile of the protein encoded

by clone HP03747.

Fig. 23 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10719.

5 Fig. 24 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10720.

Fig. 25 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded
10 by clone HP10721.

Fig. 26 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10725.

Fig. 27 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded
15 by clone HP10727.

Fig. 28 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10728.

20 Fig. 29 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10730.

Fig. 30 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded
25 by clone HP10742.

Fig. 31 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03800.

Fig. 32 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03831.

Fig. 33 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03879.

Fig. 34 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP03880.

Fig. 35 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10704.

Fig. 36 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10715.

Fig. 37 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10724.

Fig. 38 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10733.

Fig. 39 illustrates the

hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10734.

Fig. 40 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
5 by clone HP10756.

Fig. 41 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03670.

Fig. 42 illustrates the
10 hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03688.

Fig. 43 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03825

Fig. 44 illustrates the
15 hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP03877.

Fig. 45 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
20 by clone HP10765.

Fig. 46 illustrates the
hydrophobicity/hydrophilicity profile of the protein encoded
by clone HP10766.

Fig. 47 illustrates the
25 hydrophobicity/hydrophilicity profile of the protein encoded

by clone HP10770.

Fig. 48 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10772.

5 Fig. 49 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10773.

Fig. 50 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded
10 by clone HP10776.

DETAILED DESCRIPTION OF THE INVENTION

The proteins of the present invention can be obtained, for example, by a method for isolating proteins
15 from human organs, cell lines or the like, a method for preparing peptides by the chemical synthesis based on the amino acid sequences of the present invention, or a method for producing proteins by the recombinant DNA technology using the DNAs encoding the hydrophobic domains of the
20 present invention. Among these, the method for producing proteins by the recombinant DNA technology is preferably employed. For example, the proteins can be expressed in vitro by preparing an RNA by in vitro transcription from a vector having the cDNA of the present invention, and then
25 carrying out in vitro translation using this RNA as a

template. Alternatively, incorporation of the translated region into a suitable expression vector by the method known in the art may lead to expression of a large amount of the encoded protein in prokaryotic cells such as *Escherichia coli*, *Bacillus subtilis*, etc., and eukaryotic cells such as yeasts, insect cells, mammalian cells, etc.

In the case where the protein of the present invention is produced by expressing the DNA by in vitro translation, the protein of the present invention can be produced in vitro by incorporating the translated region of this cDNA into a vector having an RNA polymerase promoter, and then adding the vector to an in vitro translation system such as a rabbit reticulocyte lysate or a wheat germ extract, which contains an RNA polymerase corresponding to the promoter. The RNA polymerase promoters are exemplified by T7, T3, SP6 and the like. The vectors containing promoters for these RNA polymerases are exemplified by pKA1, pCDM8, pT3/T7 18, pT7/3 19, pBluescript II and the like. Furthermore, the protein of the present invention can be expressed in the secreted form or the form incorporated in the microsome membrane when a canine pancreas microsome or the like is added to the reaction system.

In the case where the protein of the present invention is produced by expressing the DNA in a microorganism such as *Escherichia coli* etc., a recombinant

expression vector in which the translated region of the cDNA of the present invention is incorporated into an expression vector having an origin which is capable of replicating in the microorganism, a promoter, a ribosome-binding site, a cDNA-cloning site, a terminator and the like is constructed. After transformation of the host cells with this expression vector, the resulting transformant is cultivated, whereby the protein encoded by the cDNA can be produced in large quantities in the microorganism. In this case, a protein fragment containing any translated region can be obtained by adding an initiation codon and a termination codon in front of and behind the selected translated region to express the protein. Alternatively, the protein can be expressed as a fusion protein with another protein. Only the portion of the protein encoded by the cDNA can be obtained by cleaving this fusion protein with a suitable protease. The expression vectors for *Escherichia coli* are exemplified by the pUC series, pBluescript II, the pET expression system, the pGEX expression system and the like.

In the case where the protein of the present invention is produced by expressing the DNA in eukaryotic cells, the protein of the present invention can be produced as a secretory protein, or as a membrane protein on the surface of cell membrane, by incorporating the translated region of the cDNA into an expression vector for eukaryotic

cells that has a promoter, a splicing region, a poly(A) addition site and the like, and then introducing the vector into the eukaryotic cells. The expression vectors are exemplified by pKA1, pED6dpc2, pCDM8, pSVK3, pMSG, pSVL, pBK-CMV, pBK-RSV, EBV vectors, pRS, pYES2 and the like. Examples of eukaryotic cells to be used in general include mammalian cultured cells such as monkey kidney COS7 cells, Chinese hamster ovary CHO cells and the like, budding yeasts, fission yeasts, silkworm cells, *Xenopus* oocytes and the like. Any eukaryotic cells may be used as long as they are capable of expressing the proteins of the present invention. The expression vector can be introduced into the eukaryotic cells by using a method known in the art such as the electroporation method, the calcium phosphate method, the liposome method, the DEAE-dextran method and the like.

After the protein of the present invention is expressed in prokaryotic cells or eukaryotic cells, the protein of interest can be isolated and purified from the culture by a combination of separation procedures known in the art. Examples of the separation procedures include treatment with a denaturing agent such as urea or a detergent, sonication, enzymatic digestion, salting-out or solvent precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric focusing, ion-exchange chromatography, hydrophobic

chromatography, affinity chromatography, reverse phase chromatography and the like.

The proteins of the present invention also include peptide fragments (of 5 amino acid residues or more) containing any partial amino acid sequences in the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130. These peptide fragments can be utilized as antigens for preparation of antibodies. Among the proteins of the present invention, those having the signal sequences are secreted in the form of mature proteins after the signal sequences are removed. Therefore, these mature proteins shall come within the scope of the protein of the present invention. The N-terminal amino acid sequences of the mature proteins can be easily determined by using the method for the determination of cleavage site of a signal sequence [JP-A 8-187100]. Furthermore, some membrane proteins undergo the processing on the cell surface to be converted to the secreted forms. Such proteins or peptides in the secreted forms shall also come within the scope of the protein of the present invention. In the case where sugar chain-binding sites are present in the amino acid sequences of the proteins, expression of the proteins in appropriate eukaryotic cells affords the proteins to which sugar chains are added. Accordingly, such proteins or peptides to which sugar chains are added shall also come

within the scope of the protein of the present invention.

The DNAs of the present invention include all the DNAs encoding the above-mentioned proteins. These DNAs can be obtained by using a method for chemical synthesis, a
5 method for cDNA cloning and the like.

The cDNAs of the present invention can be cloned, for example, from cDNA libraries derived from the human cells. The cDNAs are synthesized by using poly(A)⁺ RNAs extracted from human cells as templates. The human cells may
10 be cells delivered from the human body, for example, by the operation or may be the cultured cells. The cDNAs can be synthesized by using any method such as the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and
15 Hoffman, J., Gene 25: 263-269 (1983)] and the like. However, it is desirable to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)], as exemplified in Examples, in order to obtain a full-length clone in an effective manner. In addition, commercially available human cDNA libraries can
20 be utilized. The cDNAs of the present invention can be cloned from the cDNA libraries by synthesizing an oligonucleotide on the basis of base sequences of any portion in the cDNA of the present invention and screening the cDNA libraries using this oligonucleotide as a probe for
25 colony or plaque hybridization according to a method known

in the art. In addition, the cDNA fragments of the present invention can be prepared from an mRNA isolated from human cells by the RT-PCR method in which oligonucleotides which hybridize with both termini of the cDNA fragment of interest
5 are synthesized, which oligonucleotides are then used as the primers.

The cDNAs of the present invention are characterized in that they comprise any one of the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71
10 to 80, 101 to 110 and 131 to 140 or the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150. Tables 1 and 2 summarizes the clone number (HP number), the cell from which the cDNA clone was obtained, the total number of bases of the cDNA, and the
15 number of the amino acid residues of the encoded protein, for each of the cDNAs.

Table 1

SEQ ID NO.			HP number	Cell	Number of bases	Number of amino acid residues
1,	11,	21	HP03171	Thymus	2042	267
2,	12,	22	HP03424	Liver	1433	419
3,	13,	23	HP03444	Kidney	1917	415
4,	14,	24	HP03478	Umbilical cord blood	2258	380
5,	15,	25	HP03499	Kidney	1973	585
6,	16,	26	HP03500	kidney	1606	331
7,	17,	27	HP10691	Umbilical cord blood	2380	345
8,	18,	28	HP10703	Kidney	2017	89
9,	19,	29	HP10711	Kidney	1606	406
10,	20,	30	HP10712	Kidney	1695	192
31,	41,	51	HP03010	Kidney	1551	377
32,	42,	52	HP03576	Kidney	1713	81
33,	43,	53	HP03611	Kidney	1758	487
34,	44,	54	HP03612	Kidney	1550	375
35,	45,	55	HP10407	Stomach cancer	1485	350
36,	46,	56	HP10713	Kidney	2694	667
37,	47,	57	HP10714	Umbilical cord blood	3297	464
38,	48,	58	HP10716	Umbilical cord blood	2126	470
39,	49,	59	HP10717	Kidney	1781	243
40,	50,	60	HP10718	Umbilical cord blood	1788	270
61,	71,	81	HP03745	Kidney	1376	389
62,	72,	82	HP03747	Umbilical cord blood	2392	348
63,	73,	83	HP10719	Kidney	1416	261
64,	74,	84	HP10720	Kidney	1347	222
65,	75,	85	HP10721	Kidney	2284	183

Table 2

SEQ ID NO	HP number	Cell	Number of bases	Number of amino acid residues
66, 76, 86	HP10725	Kidney	1737	262
67, 77, 87	HP10727	Umbilical cord blood	1556	168
68, 78, 88	HP10728	Umbilical cord blood	1855	243
69, 79, 89	HP10730	Umbilical cord blood	2530	428
70, 80, 90	HP10742	Umbilical cord blood	1911	283
91, 101, 111	HP03800	Umbilical cord blood	1633	476
92, 102, 112	HP03831	Kidney	1095	226
93, 103, 113	HP03879	Kidney	1602	305
94, 104, 114	HP03880	Kidney	897	227
95, 105, 115	HP10704	Kidney	1866	441
96, 106, 116	HP10715	Umbilical cord blood	2198	265
97, 107, 117	HP10724	Umbilical cord blood	2180	208
98, 108, 118	HP10733	Umbilical cord blood	1527	400
99, 109, 119	HP10734	Umbilical cord blood	1905	192
100, 110, 120	HP10756	Kidney	998	260
121, 131, 141	HP03670	Umbilical cord blood	1622	337
122, 132, 142	HP03688	Umbilical cord blood	2475	236
123, 133, 143	HP03825	Kidney	1739	560
124, 134, 144	HP03877	Kidney	2005	406
125, 135, 145	HP10765	Umbilical cord blood	1558	453
126, 136, 146	HP10766	Kidney	1005	59
127, 137, 147	HP10770	Kidney	969	210
128, 138, 148	HP10772	Kidney	1241	165
129, 139, 149	HP10773	Kidney	1174	162
130, 140, 150	HP10776	Kidney	1012	221

The same clones as the cDNAs of the present invention can be easily obtained by screening the cDNA libraries constructed from the human cell lines or human

tissues utilized in the present invention using an oligonucleotide probe synthesized on the basis of the base sequence of the cDNA provided in any one of SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131 to 150.

5 In general, the polymorphism due to the individual differences is frequently observed in human genes. Accordingly, any cDNA in which one or plural nucleotides are added, deleted and/or substituted with other nucleotides in SEQ ID NOS: 11 to 30, 41 to 60, 71 to 90, 101 to 120 and 131
10 to 150 shall come within the scope of the present invention.

 Similarly, any protein in which one or plural amino acids are added, deleted and/or substituted with other amino acids resulting from the above-mentioned changes shall come within the scope of the present invention, as long as
15 the protein possesses the activity of the protein having any one of the amino acid sequences represented by SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130.

 The cDNAs of the present invention also include cDNA fragments (of 10 bp or more) containing any partial
20 base sequence in the base sequences represented by SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140 or in the base sequences represented by SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150. Also, DNA fragments consisting of a sense strand and an anti-sense
25 strand shall come within this scope. These DNA fragments can

be utilized as the probes for the genetic diagnosis.

The antibody of the present invention can be obtained from a serum after immunizing an animal using the protein of the present invention as an antigen. A peptide
5 that is chemically synthesized based on the amino acid sequence of the present invention and a protein expressed in eukaryotic or prokaryotic cells can be used as an antigen. Alternatively, an antibody can be prepared by introducing the above-mentioned expression vector for eukaryotic cells
10 into the muscle or the skin of an animal by injection or by using a gene gun and then collecting a serum therefrom (JP-A 7-313187). Animals that can be used include a mouse, a rat, a rabbit, a goat, a chicken and the like. A monoclonal antibody directed to the protein of the present invention
15 can be produced by fusing B cells collected from the spleen of the immunized animal with myelomas to generate hybridomas.

In addition to the activities and uses described above, the polynucleotides and proteins of the present invention may exhibit one or more of the uses or biological
20 activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as,
25 for example, in gene therapies or vectors suitable for

introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein

(such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell '75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation

Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol.

145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

5 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current Protocols in Immunology. J.E.e.a. Coligan
10 eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

15 Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In Current Protocols in Immunology.
20 J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6-
25 Nordan, R. In Current Protocols in Immunology. J.E.e.a.

Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In
5 Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John
10 Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include,
15 without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines
20 and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

25: Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune

pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by

the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant.

Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate

activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy.

Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function
5 may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be
10 enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing
15 the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a
20 portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

In another application, up regulation or
25 enhancement of antigen function (preferably B lymphocyte

antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a

cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19;

Chapter 7, Immunologic studies in Humans); Herrmann et al.,
Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et
al., J. Immunol. 128:1968-1974, 1982; Handa et al., J.
Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol.
5 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512,
1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-
2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974,
1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai
et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J.
10 Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512,
1988; Bertagnolli et al., Cellular Immunology 133:327-341,
1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin
responses and isotype switching (which will identify, among
15 others, proteins that modulate T-cell dependent antibody
responses and that affect Th1/Th2 profiles) include, without
limitation, those described in: Maliszewski, J. Immunol.
144:3028-3033, 1990; and Assays for B cell function: In
vitro antibody production, Mond, J.J. and Brunswick, M. In
20 Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1
pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will
identify, among others, proteins that generate predominantly
Th1 and CTL responses) include, without limitation, those
25 described in: Current Protocols in Immunology, Ed by J. E.

Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W
Strober, Pub. Greene Publishing Associates and Wiley-
Interscience (Chapter 3, In Vitro assays for Mouse
Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies
5 in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986;
Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et
al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will
identify, among others, proteins expressed by dendritic
10 cells that activate naive T-cells) include, without
limitation, those described in: Guery et al., J. Immunol.
134:536-544, 1995; Inaba et al., Journal of Experimental
Medicine 173:549-559, 1991; Macatonia et al., Journal of
Immunology 154:5071-5079, 1995; Porgador et al., Journal of
15 Experimental Medicine 182:255-260, 1995; Nair et al.,
Journal of Virology 67:4062-4069, 1993; Huang et al.,
Science 264:961-965, 1994; Macatonia et al., Journal of
Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al.,
Journal of Clinical Investigation 94:797-807, 1994; and
20 Inaba et al., Journal of Experimental Medicine 172:631-640,
1990.

Assays for lymphocyte survival/apoptosis (which
will identify, among others, proteins that prevent apoptosis
after superantigen induction and proteins that regulate
25 lymphocyte homeostasis) include, without limitation, those

described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or

erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complementary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

25. Suitable assays for proliferation and

differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without
5 limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those
10 described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New
15 York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I.
20 Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New
25 York, NY. 1994; Long term bone marrow cultures in the

presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth

repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful
5 in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

10 Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue
15 is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to
20 tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the
25 repair of congenital, trauma induced, or other tendon or

ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and
5 cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to
10 promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds and the like.

It is expected that a protein of the present
15 invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for
20 promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

25 A protein of the present invention may also be

useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

5. A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of

follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et

al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have
5 chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to
10 mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes,
15 monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly
20 or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing
25 such protein or peptide in any known assay for cell

chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will
5 identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for
10 movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta
15 Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such
25 as hemophilias) or to enhance coagulation and other

hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions
5 resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke)).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity
10 include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

15 Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without
20 limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their
25 ligands) and receptor/ligand pairs involved in antigen

presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity

may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

20 Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly

(such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or cardiac cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other

nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Examples

The present invention is specifically illustrated in more detail by the following Examples, but Examples are not intended to restrict the present invention. The basic procedures with regard to the recombinant DNA and the enzymatic reactions were carried out according to the literature ["Molecular Cloning. A Laboratory Manual", Cold

Spring Harbor Laboratory, 1989]. Unless otherwise stated, restriction enzymes and various modifying enzymes to be used were those available from Takara Shuzo. The buffer compositions and the reaction conditions for each of the enzyme reactions were as described in the attached instructions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

(1) Selection of cDNAs Encoding Proteins Having Hydrophobic Domains

Human liver cDNA library (WO 98/21328) and human stomach cancer cDNA library (WO 98/21328), as well as the cDNA libraries constructed from human kidney mRNA (Clontech), human thymus mRNA (Clontech) and human umbilical cord blood mRNA were used as cDNA libraries.

Full-length cDNA clones were selected from the respective libraries and the whole base sequences thereof were determined to construct a homo-protein cDNA bank consisting of the full-length cDNA clones. The hydrophobicity/hydrophilicity profiles were determined for the proteins encoded by the full-length cDNA clones registered in the homo-protein cDNA bank by the Kyte-Doolittle method [Kyte, J. & Doolittle, R. F., J. Mol. Biol. 157: 105-132 (1982)] to examine the presence or absence of a hydrophobic domain. A clone that has a hydrophobic region

being assumed as a secretory signal or a transmembrane domain in the amino acid sequence of the encoded protein was selected as a clone candidate.

(2) Protein Synthesis by In Vitro Translation

5 The plasmid vector bearing the cDNA of the present invention was used for in vitro transcription/translation with a T_NT rabbit reticulocyte lysate kit (Promega). In this case, [³⁵S]methionine was added to label the expression product with a radioisotope. Each of the reactions was
10 carried out according to the protocols attached to the kit. Two micrograms of the plasmid was subjected to the reaction at 30°C for 90 minutes in the reaction solution of a total volume of 25 µl containing 12.5 µl µ of T_NT rabbit reticulocyte lysate, 0.5 µl of a buffer solution (attached
15 to the kit), 2 µl of an amino acid mixture (without methionine), 2 µl of [³⁵S]methionine (Amersham) (0.37 MBq/µl), 0.5 µl of T7 RNA polymerase, and 20 U of RNasin. The experiment in the presence of a membrane system was carried out by adding 2.5 µl of a canine pancreas microsome fraction
20 (Promega) to the reaction system. To 3 µl of the reaction solution was added 2 µl of the SDS sampling buffer (125 mM Tris-hydrochloride buffer, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0.025% bromophenol blue and 20% glycerol) and the resulting mixture was heated at 95°C for 3 minutes
25 and then subjected to SDS-polyacrylamide gel electrophoresis.

The molecular weight of the translation product was determined by carrying out the autoradiography.

(3) Expression in COS7

Escherichia coli cells harboring the expression vector for the protein of the present invention were cultured at 37°C for 2 hours in 2 ml of the 2 x YT culture medium containing 100 µg/ml of ampicillin, the helper phage M13KO7 (50 µl) was added thereto, and the cells were then cultured at 37°C overnight. Single-stranded phage particles were obtained by polyethylene glycol precipitation from a supernatant separated by centrifugation. The particles were suspended in 100 µl of 1 mM Tris-0.1 mM EDTA, pH 8 (TE).

The cultured cells derived from monkey kidney, COS7, were cultured at 37°C in the presence of 5% CO₂ in the Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal calf serum. 1 x 10⁵ COS7 cells were inoculated into a 6-well plate (Nunc, well diameter: 3 cm) and cultured at 37°C for 22 hours in the presence of 5% CO₂. After the medium was removed, the cell surface was washed with a phosphate buffer solution followed by DMEM containing 50 mM Tris-hydrochloride (pH 7.5) (TDMEM). A suspension containing 1 µl of the single-stranded phage suspension, 0.6 ml of the DMEM medium and 3 µl of TRANSFECTAM™ (IBF) was added to the cells and the cells were cultured at 37°C for 3 hours in the presence of 5% CO₂. After the sample solution was removed,

the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf serum was added, and the cells were cultured at 37°C for 2 days in the presence of 5% CO₂. After the medium was exchanged for a medium containing
5 [35S]cysteine or [35S]methionine, the cells were cultured for one hour. After the medium and the cells were separated each other by centrifugation, proteins in the medium fraction and the cell membrane fraction were subjected to SDS-PAGE.

(4) Preparation of Antibodies

10 A plasmid vector containing the cDNA of the present invention was dissolved in a phosphate buffer solution (PBS: 145 mM NaCl, 2.68 mM KCl, 8.09 mM Na₂HPO₄, 2 mM KH₂PO₄, pH 7.2) to a concentration of 2 µg/µl. 25 µl each (a total of 50 µl) of the thus-prepared plasmid solution in
15 PBS was injected into the right and left musculi quadriceps femoris of three mice (ICR line) using a 26 gauge needle. After similar injections were repeated for one month at intervals of one week, blood was collected. The collected blood was stored at 4°C overnight to coagulate the blood,
20 and then centrifuged at 8,000 x g for five minutes to obtain a supernatant. NaN₃ was added to the supernatant to a concentration of 0.01% and the mixture was then stored at 4°C. The generation of an antibody was confirmed by immunostaining of COS7 cells into which the corresponding
25 vector had been introduced or by Western blotting using a

cell lysate or a secreted product.

(5) Clone Examples

<HP03171> (SEQ ID NOS: 1, 11 and 21)

Determination of the whole base sequence of the
5 cDNA insert of clone HP03171 obtained from cDNA library of
human thymus revealed the structure consisting of a 90-bp
5'-untranslated region, a 804-bp ORF, and a 1148-bp 3'-
untranslated region. The ORF encodes a protein consisting of
267 amino acid residues and there existed one putative
10 transmembrane domain. Figure 1 depicts the
hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of 34 kDa that was somewhat larger than the molecular weight
of 30,234 predicted from the ORF. In this case, the
15 addition of a microsome led to the formation of a product of
38 kDa. In addition, there exists in the amino acid sequence
of this protein one site at which N-glycosylation may occur
(Asn-Thr-Thr at position 169).

20 The search of the protein database using the amino
acid sequence of the present protein revealed that the
protein was similar to chicken putative transmembrane
protein E3-16 (Accession No. AAB70816). Table 3 shows the
comparison between amino acid sequences of the human protein
25 of the present invention (HP) and chicken putative

transmembrane protein E3-16 (GG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.0% in the entire region.

Table 3

10	HP MVKISFQPAVAGIKGDKADKASAPAPASATEILLTPAREEQPPQHRSKRGSSVGGVCY
	***.**.*.* . *.*..... . *. *.*... .. *
	GG MVKVSFNSALAH--KEAANKKEENSQVL-ILPPDAKEPEDVVVPAGHKRAWCWCW--CF
	HP LSMGMVLLMGLVFASVYIYRYFFLAQLARDNFFRCGVLY-EDSL-----SSQVRTQM--
15	*.. *.*.....*.*.** ..* .*.**.* **.* ..*.....
	GG --GLAFMLAGVILGGAYLYKYFAFQQ--GGVYF-CGIKYIEDGLSLPESGAQLKSARYH
	HP ELEEDVKIYLDENYERINVPVPQGGGDPADIIHDFQRGLTAYHDISLDKCYVIELNTTI
	..*....* .*. *.*.****.*...****.* **.* ****.* ****.* **.*..
20	GG TIEQNIQILEEEDVEFISVPVPEFADSDPADIVHDFHRRLTAYLDLSLDKCYVIPLNTSV
	HP VLPPRNFWELLMNVKRGTYLPQTYIIQEEMVTEHVSDKEALGSFIYHLCNGKDTYRLRR
	*.**.* **.*.* ****.*.*.*.*.* **.*... ..** **.* **.* **.*.*
	GG VMPPKNFLELLINIKAGTYLPQSYLIHEQMIVTDRIENVDDLGGFFIYRLCRGKETYLQR
25	

HP RATRRRINKRGAKNCNAIRHFENTFVVETLICGVV

..... *.**.* **. ***** *.*****

GG KEAMKGIQKREAVNCRKIRHFENRFAMETLICEQ

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AL036384) among ESTs.

10 However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03424> (SEQ ID NOS: 2, 12 and 22)

Determination of the whole base sequence of the
15 cDNA insert of clone HP03424 obtained from cDNA library of human liver revealed the structure consisting of a 4-bp 5'-untranslated region, a 1260-bp ORF, and a 169-bp 3'-untranslated region. The ORF encodes a protein consisting of 419 amino acid residues and there existed a putative
20 secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 2 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product
25 of 50 kDa that was somewhat larger than the molecular weight

of 46,375 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 54 kDa. In addition, there exist in the amino acid sequence of this protein six sites at which N-glycosylation may occur
5 (Asn-Ala-Ser at position 29, Asn-Val-Thr at position 40, Asn-Cys-Thr at position 112, Asn-Lys-Ser at position 135, Asn-Ile-Ser at position 172 and Asn-Phe-Ser at position 189). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to
10 expect that the mature protein starts from aspartic acid at position 28.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Drosophila melanogaster* GOLIATH
15 protein (Accession No. Q06003). Table 4 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Drosophila melanogaster* GOLIATH protein (DM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that
20 of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 40.8% in the intermediate region of 218 amino acid residues.

25

Table 4

	HP MSCAGRAGPARLAALALLTCSLWPARADNASQEYYTALINVTVQEPGRGAPLTFRIDRGR	
5	HP YGLDSPKAEVRGQVLAPLPLHGVADHLGCDPQTRFFVPPNIKQWIALLRGNCTFKEKIS	
	HP RAAFHNAVAVVIYNNKSKEEPVTMTHPGTGDIIVMITELRGKDILSYLEKNISVQMTIA	
		* * * * *
	DM MQLEKMQIKGKTRNIAAVITYQNIGQDLSLTLDKGYNTISII	
10	HP VGTR--MPPKNFSRGS�VFVSISFIVLMISSAWLIFYFIQKIRYTNARDRNQRRLGDA	
		* * * * *
	DM EGRRGVRTISSLNRTSVLFVSISFIVDDIL--CWLIFYIQRFRYMQAKDQQSRNLCSVT	
15	HP KKAISKLTTRTVKKGDKETDPDFDHCAVCIESYQNDVVRILPCKHVFHKSCVDPWLSEH	
		* * * * *
	DM KKAIMKIPTKTGKFS--EKDLDSDCCAICIEAYKPTDTIRILPCKHEFHKNCIDPWLIEH	
	HP CTCPMCKLNILKALGIVPNLPCTDNVAFDMERLRTQAVNRRSALGDLAGDNSLGLLEPLR	
20		* * * * *
	DM RTCPMCKLDVLKFYGYVVGDIYQTPS--PQHTAPIASIEEVPVIVVAVPHGPQLQLQ	
	HP TSGISPLPDGELTPRTGEINIAVTKEWFIIASFGLLSALTLCYMIIRATASLNANEVEW	
		* * * * *
25	DM ASNMSSFAPSHYFQSSRSPSSSVQQQLAPLTYQPHPQQAASERGRNRNSAPATMPHAITAS	

HP F

DM HQVTDV

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA082118) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03444> (SEQ ID NOS: 3, 13 and 23)

15 Determination of the whole base sequence of the cDNA insert of clone HP03444 obtained from cDNA library of human kidney revealed the structure consisting of a 209-bp 5'-untranslated region, a 1248-bp ORF, and a 460-bp 3'-untranslated region. The ORF encodes a protein consisting of 20 415 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 3 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product 25 of 43 kDa that was somewhat smaller than the molecular

weight of 45,691 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 42 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamine at position 24.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human type I procollagen C-proteinase enhancer protein (Accession No. BAA23281). Table 5 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human type I procollagen C-proteinase enhancer protein (CP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.6% in the entire region.

Table 5

HP	M R G A N A W A P L C L L L A A A T Q L S R Q Q S P E R P V F T C G G I L T G E S C F I G S E G F P G V Y P
	* ** . * * **** ** . **** . . ***** . **
CP	M L P A A T A S L L G P L L T A C A L L P F A - Q - G Q T P N Y T R P V F L C G G D V K G E S G Y V A S E G F P N L Y P

HP PNSKCTWKITVPEGKVVLNFRFIDLESDNLCRYDFVDVYNHG-ANGQRIGRFCGTFRPG

. *.*.**. * *.** .***. ***** .*. * .***.*****.

CP PNKECIWTITVPEGQTVSLSRVFDLELHPACRYDALEVFAGSGTSGQRLGRFCGTFRPA

5 HP ALVSSGNKMMVQMISDANTAGNGFMAMFSAAEPNERGDQYCGLLDRPSGSFKTPNWPDR

..**..**.. ..*..*..*..**.. ..*.. ..*..*** *.. *..*****..

CP PLVAPGNQVTLRMTTDEGTGGRGFLWYSGRATSGTEHQFCGGRLEKAQGTLTTPNWPES

HP DYPAGVTCVWHIVAPKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGD

10 ***. *. * ***. ** . *. *. *. *****. *. *. *****. *. *****. . *. **. **. ****

CP DYPPGISCSWHIIAPPDQVIALTFEKFDLEPDTCRYDSVSFNGAVSDDSRRLGKFCGD

HP SPPAPIVSEARNELLIQFLSDLSLTADGFIGHYIFRPKKLPITTE-----

. * . * ** ***** . ** . ***** . ***** . * *

15 CP AVPGSISSEGNELLVQFVSDLSVTADGFSASYKTLPRGTAKGQGP GPKRGTEPKVKLPP

HP QPVTTFPVTGLKTTVALCQQKCRRTGTLEGNYCSSDFVLAGTVITTITRDG-SLHATV

..... *.....**.....*.....**.....*.....**.....

CP KSQPPEKTEESPSAPDAPTCPKQCRRTGTLQSNFCASSLVVTATVKSMVREPGGLAVTV

20

HP SIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRRGLNYIIMGQVGEDGRGKIM-PNSF

..*.*.*.....*...******...*.*.******.*.*..**..*.*

CP SLIGAYKTGGLDLSPPTGASLKFYVPCKQCPPMKKGVSYLLMGQV-EENRGPVLPPEF

25- HP IMFKTKNQKLLDALKNKQC

.....*..*.....*
CP VVLRPNQDQILTNL SKRK CPSQPVRAAASQD

5 The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. D78874) among ESTs. However, since they are
partial sequences, it can not be judged whether or not they
10 encode the same protein as the protein of the present
invention.

<HP03478> (SEQ ID NOS: 4, 14 and 24)

Determination of the whole base sequence of the
cDNA insert of clone HP03478 obtained from cDNA library of
15 human umbilical cord blood revealed the structure consisting
of a 224-bp 5'-untranslated region, a 1143-bp ORF, and a
891-bp 3'-untranslated region. The ORF encodes a protein
consisting of 380 amino acid residues and there existed five
putative transmembrane domains. Figure 4 depicts the
20 hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of high molecular weight.

25 The search of the protein database using the amino
acid sequence of the present protein revealed that the

Table 6

15 HP MLQTLYDYFWWERLWLPVNLTWADLEDGRVYAKASDLYITLPLALLFLIVRYFFEL
 . * . ** . ** * . *** ***** . ** ** . * . ** . * . * . *
 HR MDLLMDLYHWFWNEKFWLPQNLTWEDLKRTEEKQFGETRDLWLTFLPLCITVLCIRFSVEK
 HP YVATPLAALLNIKEKTRLRAPPNATLEHFYLTSGKQPKQVEVELLSRQSGLSGRQVERWF
 . * ** . ** . * * . ** . * * . . . * . ** * . * . * **
 20 HR GIARPLGKWLNLSERLHTPPRENIVLEKVKYKTITRKPYSQVEDLCKQTGWRKHEINVWF
 HP RRRRNQDRPSLLKKFREASWRFTFYLIAFIAGMAVIVDKPWFYDMKKVWEGYPIQSTIPS
 * ** . * . ** . * . *** . *** . * . * . * . * . . . * . . . **
 HR RKKNLVGRPTTLTKFQETFWRFAYLTSFFYGLYVMYDQECVWQTEKCFSNYPEDHVLSQ
 25

HP Q-YWYYMIELSFYWSLLFSIASDVKRKDFKEQIIHHVATIILISFSWFANYIRAGTLIMA

. *. ** . *** . ** ***** * . *** . *** . . * . *** . * . * . .

HR KIYYYYLIELAFYSATTLTQFFDVKRKDFWEMFIHHIVTIILLCGSYTLNYTKMGAFILV

5 HP LHDSSDYLLESAKMFNYAGWKNTCNNIFIVFAIVFIITRLVILPFWILHCTLVYPLELYP

. *** . * . * *** . ** . . . * ** * . * ***** . ** . . . * . . *

HR VHDSADFYIEFAKMGKYANNSLVTVNGFISFTISFFLSRLVILPLWIVPSIWFYGIYTYN

HP AFFGYFFNSMMGVLQLLHIFWAYLILMAHKFITGKLVEDERSDREETESSEGEAAAAG

10 . . . * ***** . * * . . * . * . . . * * * . . .

HR CAMA-WLFCALL-ILQLLHFYWFHIVKAAAYASILVGVIERDTRSESEDSSAEDETAKYS

HP GGAKSRLANGHPILNNNHRKND

*

15 HP VGSGDYTESNGIHKRVVTAR

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T27334) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

25 <HP03499> (SEQ ID NOS: 5, 15 and 25)

Determination of the whole base sequence of the cDNA insert of clone HP03499 obtained from cDNA library of human kidney revealed the structure consisting of a 129-bp 5'-untranslated region, a 1758-bp ORF, and a 86-bp 3'-untranslated region. The ORF encodes a protein consisting of 585 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 5 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 63 kDa that was almost identical with the molecular weight of 63,987 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 82 kDa. In addition, there exist in the amino acid sequence of this protein five sites at which N-glycosylation may occur (Asn-Ile-Thr at position 89, Asn-Glu-Thr at position 106, Asn-Ala-Thr at position 189, Asn-Arg-Thr at position 220 and Asn-Ala-Thr at position 315).

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to Chinese hamster hypothetical protein 2BE2121 (Accession No. A30227). Table 7 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and Chinese hamster hypothetical protein 2BE2121 (CH). Therein, the marks of -,

*, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a
 5 homology of 44.8% in the entire region.

Table 7

	HP	MVCREQLSKNQVKWVFAGITCVSVVVIAAIVLAITLRRPGCELEACSPDADMLDYLLSLG	
10			...***.*.
	CH		SWSENILDYFLRNS
	HP	QISRRDALEVTWYHAANSKKAMTAALNSNITVLEADVNV EGLGTANETGVPIMAHPTIY	
		.*.*.***.*.*.***.*.****.*.*.*****.	
15	CH	QITTEDGAEIIWYHAANHKSQMQEALRSAAHMIEADVLLPS--DGSEHGQPIMAHPPEN	
	HP	SDNTLEQWLDAVLGSSQKGIKLDFKNIKAVGPSLDLLRQLTEEGKVRRIWINADILKGP	
		*****.*.*.*.*.*.*****.*.*.*.*.*.*.*.***.*.*	
	CH	SDNTLQEWLAEVM-KSNKGIKLDFKSLAAARASMLFLDNVKQH--LQCPVWMNADVLPGP	
20			
	HP	NMLISTEVNATQFLALVQEKYPKATLSPGWTTFY MSTSPNRTYTQAMVEKMHEL VGGVPQ	
		..*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*	
	CH	NG-SSKVVDAKAFLDTVTSFFPDVTFSLGWTTGWHPEK VNEGYSWTMVKEMDYICSLTQ	
25	HP	RVTFPVRSSMVRAAWPHFSWLLSQSERYSLTLWQAASDPMSVEDLLYVRDNTAVHQVYYD	

*****...**... ***...*****.*...*...*****.**... **.**
 CH PVTFPVRAALVRQSCSQLLWLLKKSNRYSLTVWTGKDDSYPTEDLLYIRDYFNKTQVFYD
 HP IFEPLLSQFKQLALNATRKPYYTGGSLLIPLLQLPGDDGLNVEWLVPDVQGSCKTATMTL
 5 *.** ***
 CH ILEPQSHEFKQAIGI

Furthermore, the search of the GenBank using the
 10 base sequences of the present cDNA has revealed the
 registration of sequences that shared a homology of 90% or
 more (for example, Accession No. R92398) among ESTs. However,
 since they are partial sequences, it can not be judged
 whether or not they encode the same protein as the protein
 15 of the present invention.

<HP03500> (SEQ ID NOS: 6, 16 and 26)

Determination of the whole base sequence of the
 cDNA insert of clone HP03500 obtained from cDNA library of
 human kidney revealed the structure consisting of a 134-bp
 20 5'-untranslated region, a 996-bp ORF, and a 476-bp 3'-
 untranslated region. The ORF encodes a protein consisting of
 331 amino acid residues and there existed one putative
 transmembrane domain at the N-terminus. Figure 6 depicts the
 hydrophobicity/hydrophilicity profile, obtained by the Kyte-
 25 Doolittle method, of the present protein. In vitro

translation resulted in formation of a translation product of 38 kDa that was almost identical with the molecular weight of 37,694 predicted from the ORF.

5 The search of the protein database using the amino acid sequence of the present protein revealed that the amino acid sequence of the protein matched with that of human hypothetical protein (Accession No. AAC05803) in which a region of 62 amino acid residues from glycine at position 88 to lysine at position 149 was deleted.

10 The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA340631) among ESTs. However, since they are partial sequences, it can not be judged whether or not they
15 encode the same protein as the protein of the present invention.

<HP10691> (SEQ ID NOS: 7, 17 and 27)

20 Determination of the whole base sequence of the cDNA insert of clone HP10691 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 246-bp 5'-untranslated region, a 1038-bp ORF, and a 1096-bp 3'-untranslated region. The ORF encodes a protein consisting of 345 amino acid residues and there existed at least two putative transmembrane domains. Figure 7 depicts
25 the hydrophobicity/hydrophilicity profile, obtained by the

Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human BB1 protein (Accession No. AAB37433). Table 8 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human BB1 protein (BB). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The C-terminal region of 215 amino acid residues of the present protein shared a homology of 81.9% with the N-terminal region of human BB1 protein.

Table 8

	HP	MSPEWTYLVLLISIPIGFLFKAGPGLKRWGAAVGLGLTLFTCGPHTLHSLVTILGT	
20			
	HP	WALIQAQPCSCHALALAWTFSYLLFFRALSLLGLPTPTPFTNAVQLLLTLKLVSLASEVQ	
	HP	DLHLAQRKEMASGFSKGPTLGLLPDVPSLMETLSYSYCYVGIMTGPFTRYTYLDWLEQP	
		*****	..*..*..*..*
25	BB	MASGFSKGPTLGLLRRALPDGDT-QLQLLLRGNHDPVLPPLPPLAGAA	

HP FPGAVPSLRPLLRRRAWPAPLFGLLFLSSHLFPLEAVREDAFYARPLPARLFYMIPVFFA

* . . .*****

BB LPRGSASLRPLLRRRAWPAPLFGLLFLSSHLFPLEAVREDAFYARPLPARLFYMIPVFFA

5

HP FRMRFYVAWIAAECGCIAAGFGAYPVAAKARAGGGPTLQCPPSSPEKAASLEYDYETIR

BB FRMRFYVAWIAAECGCIAAGFGAYPVAAKARAGGGPTLQCPPSSPEKAASLEYDYETIR

10

HP NIDCYSTDFCVRVRDGMRYWNMTVQWWLAQYIYKSAPARSYVLRL

BB NIDCYSTDFCVRVRDGMRYWNMTVQWWLAQYIYKSAPARSYVLRTAWTMLLSAYWHGLHP

15

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W48653) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

20

<HP10703> (SEQ ID NOS: 8, 18 and 28)

Determination of the whole base sequence of the cDNA insert of clone HP10703 obtained from cDNA library of human kidney revealed the structure consisting of a 359-bp

25

5'-untranslated region, a 270-bp ORF, and a 1388-bp 3'-untranslated region. The ORF encodes a protein consisting of 89 amino acid residues and there existed one putative transmembrane domain. Figure 8 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 18 kDa that was larger than the molecular weight of 10,469 predicted from the ORF.

10 The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T08343) among ESTs. However, since they are partial sequences, it can not be judged whether or not they
15 encode the same protein as the protein of the present invention.

 <HP10711> (SEQ ID NOS: 9, 19 and 29)

 Determination of the whole base sequence of the cDNA insert of clone HP10711 obtained from cDNA library of
20 human kidney revealed the structure consisting of a 29-bp 5'-untranslated region, a 1221-bp ORF, and a 356-bp 3'-untranslated region. The ORF encodes a protein consisting of 406 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative
25 transmembrane domain at the N-terminus. Figure 9 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 44 kDa that was almost identical with the molecular weight of 43,836 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 58 kDa. In addition, there exist in the amino acid sequence of this protein seven sites at which N-glycosylation may occur (Asn-Ser-Thr at position 65, Asn-Trp-Ser at position 95, Asn-Val-Ser at position 134, Asn-Ile-Thr at position 159, Asn-Gly-Ser at position 187, Asn-Arg-Ser at position 230 and Asn-Leu-Thr at position 333). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamic acid at position 36.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse kidney predominant protein (Accession No. BAA92527). Table 9 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse kidney predominant protein (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The

both proteins shared a homology of 79.9% in the entire region.

Table 9

5

HS MRGSVECTWGWGHCAPSPLLLWTLFFFAPFGLLGEKTRQVSLEVIPNWLGPLQNLLHIR

* *** .***.* ** **. ***** **.*****.***.* * *****

MM MFRCWGPWGWVPCAPTPWLLLSLLVCSAPFGLQGEETRQVSMEVISGWPNP-QNLLHIR

10

HS AVGTNSTLHYVWSSLGPLAVVMVATNTPHSTLSVNWSLLLSPEPDGGLMVLPKDSIQFSS

.**.***.*****.*.*****.***.*****.*****

MM AVGSNSTLHYVWSSLGPPAVVLVATNTTQSVLSVNWSLLLSPPDPAGALMVLPKSSIQFSS

15

HS ALVFTRLLEFDSTNVSDTAAKPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHMND

*****.*.***.*.*****.*****.***.*.***.***.*.*

MM ALVFTRLLEFDSTNASE-GAQPPGKPYPPYSLAKFSWNNITNSLDLANLSADFQGRPVD

HS PTRTFANGSLAFRVQAFSRSSRPAQPPRLLHTADTCQLEVALIGASPRGNRSLFGLEVAT

** .*****.*.*****.*****.*****.*****.*****

20

MM PTGAFANGSLTFKVQAFSRSGRPAQPPRLLHTADVCQLEVALVGASPRGNHSLFGLEVAT

HS LGQGPDCPSMQEQHSIDDEYAPAVFQLDQLLWGSLPSGFAQWRPVAYSQKPGGRESALPC

*****.*.*****.*****.*****.*****.*.*****

MM LGQGPDCPSVNERNSIDDEYAPAVFQLNQLLWGSSPSGFMQWRPVAFSEERAREALPC

25

MM QASTLHSTLASSLPHSPIVQAFFGSQNNFCAFNLTFGAPTGPGYWDQYYLCWSMLLGMGF

*****.*****.***** *****,*.,*****

MM PPVDIFSPLVLGIMAVLGA~~PGLMFLGGFL~~LLLRHRRYSEYQSIN

10 The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. AA362394) among ESTs. However, since they are
partial sequences, it can not be judged whether or not they
15 encode the same protein as the protein of the present
invention.

<HP10712> (SEQ ID NOS: 10, 20 and 30)

Determination of the whole base sequence of the cDNA insert of clone HP10712 obtained from cDNA library of human kidney revealed the structure consisting of a 52-bp 5'-untranslated region, a 579-bp ORF, and a 1064-bp 3'-untranslated region. The ORF encodes a protein consisting of 192 amino acid residues and there existed four putative transmembrane domains. Figure 10 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse calcium channel gamma 5 subunit (Accession No. CAB86387). Table 10 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse calcium channel gamma 5 subunit (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 75.0% in the entire region.

Table 10

	HS	MTAVGVQAQRPLGQRQPRRSFFESFIRTLIITCVALAVVLSSVSICDGHWLLAEDRLFGL
20		***.*.**..**..*.*****.*****.***.***
	MM	MTAIGAQAHKLLGLKRPHRSFFESFIRTLIIVCTALAVVLSSVSICDGHWLLVEDHLFGL
	HS	WHFCTTTNQSVPICFRDLGQAHVPG LAVGMGLVRSVGALAVVAAIFGLEFLMVSQLCEDK
		..*.***.*.*.*.***.***.*****.***.*.*****.*.***.***
25	MM	WYFCTIGNHSEPHCLRDLSQAHPGLAVGMGLARSVAAMAVVAAIFGLEMLIVSQCEDV

HS HSQCKWVMGSILLVSVFLSSGGLLG FVILLRNQVTLIGFTLMFWCEFTASFLFLNAIS

. *. **..** ****. *. *****. *. ***. **..*. *****. **** *

MM RSRRKWAIGSYLLLVAFILSSGGLLTFIILLKNQINLLGFTLMFWCEFTASFLFLNAAS

5

HS GLHINSITHPWE

*****. *. **.

MM GLHINSLTQPWDPAGTLAYRKRGYDGTSLI

10

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA910339) among ESTs.

15 However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03010> (SEQ ID NOS: 31, 41 and 51)

20 Determination of the whole base sequence of the cDNA insert of clone HP03010 obtained from cDNA library of human kidney revealed the structure consisting of a 97-bp 5'-untranslated region, a 1134-bp ORF, and a 320-bp 3'-untranslated region. The ORF encodes a protein consisting of 377 amino acid residues and there existed at least eight
25 putative transmembrane domains. Figure 11 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 42 kDa that was almost identical with the molecular weight of 41,462 predicted from the ORF as well as a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Arabidopsis thaliana* hypothetical protein (Accession No. AAC34490). Table 11 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Arabidopsis thaliana* hypothetical protein (AT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 42.0% in the entire region other than the N-terminal region.

Table 11

HP MDSALSDPHNGSAEAGGPTNSTTRPPSTPEGIALAYGSLLLMALLPIFFGALRSVRCARG

***.

25 AT

MKN CERFANLALAGLTLAPLVVRVNPNLNVILTACITVYVGCFRS

HP KNASDMPETITSRDAARFPIIASCTLLGLYLFFKIFSQEYINLLLSMYFFVLGILALSH

. . . ** . . * **** . . * ** . * . * . * . * . * . ***** **** *

AT VKDTPPTETMSKEHAMRFPLVGSAMLLSLFLLFKFLSKDLVNAVLTAYFFVLGIVALSAT

HP ISPFMNKFFPASFPNRQYQLLFTQCSGENKEEII NYEFDTKDLVCLGLSSIVGVWYLLRK

. * . . . * * * . . . ** * ** . *

AT LLPAIRRFLPNPWNDNLIVWRF-----PYFKSLEVEFTKSQVVAGIPGTFFCAWYAWKK

10 HP HWIANNLFGSLNGVELLHLNNVSTGCILLGGLFIYDVFVFGTNYMVTYAKSFEAPI

..***.*..*.*.*.*..***.***.***.***.***.*.***.***.***.***

AT HWLANNILGLSFCIQGIEMLSLGSFKTGAILLAGLFFYDIFWVFFTPVMVSVAKSFDAP1

HP KLVFPQDLLEKGLEANNFAMLGLDVVIPGIFIALLLRFDISLKKNTHTYFYTSFAAYIF

15 **. ** . . . * . . . *****. *****. ** *****. * ** . . . *

AT KLLFPTG---DALRP--YSMLGLGDIVIPGIFVALALRFDVSRRRQPQ-YFTSAFIGYAV

HP GLGLTIFIMHIFKHAQPALLYLVPACIGFPVLVALAKGEVTEMFSYEESNPKDPAAVTES

*. ***. *. *. *****. ****. ***. . *. ** . * . **

20 AT GVILTIVVMNWFQAAQPALLYIVPAVIGFLASHCIWNGDIKPLLAFFDESKTEE-ATTDES

HP KEGTEASASKGLEKKEK

* * *

AT KTSEEVNKAHDE

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA380429) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03576> (SEQ ID NOS: 32, 42 and 52)

Determination of the whole base sequence of the cDNA insert of clone HP03576 obtained from cDNA library of human kidney revealed the structure consisting of a 88-bp 5'-untranslated region, a 246-bp ORF, and a 1379-bp 3'-untranslated region. The ORF encodes a protein consisting of 81 amino acid residues and there existed two putative transmembrane domains. Figure 12 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 20 kDa that was larger than the molecular weight of 9,178 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human vacuolar proton ATPase 9 kDa (Accession No. NP_003936). Table 12 shows the comparison

between amino acid sequences of the human protein of the present invention (HP) and human vacuolar proton ATPase 9 kDa (VP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 71.2% in the entire region.

10 Table 12

HP MTAHSFALPVIIFTTFWGLVGIAGPWFVPKGPNRGVIITMLVATAVCCYFLWLIAILAQL

*. *. *. ***. **. ***. *****. *****

VP MAYHGLTVPLIVMSVFWGFVGFVLPWFIPKGPNRGVIITMLVTCVCCYFLWLIAILAQL

15

HP NPLFGPQLKNETIWYVRFLWE

*****... *

VP NPLFGPQLKNETIWYLKYHWP

20

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W22566) among ESTs. However, since they are partial sequences, it can not be judged

whether or not they encode the same protein as the protein of the present invention.

<HP03611> (SEQ ID NOS: 33, 43 and 53)

Determination of the whole base sequence of the cDNA insert of clone HP03611 obtained from cDNA library of human kidney revealed the structure consisting of a 189-bp 5'-untranslated region, a 1464-bp ORF, and a 105-bp 3'-untranslated region. The ORF encodes a protein consisting of 487 amino acid residues and there existed eleven putative transmembrane domains. Figure 13 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human cystine/glutamate transporter (Accession No. BAA82628). Table 13 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human cystine/glutamate transporter (CG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology

Table 13

[illegible]

HP QAVAVTFGDRVLYPASWIVPLFVAFSTIGAANGTCFTAGRLIYVAGREGHMLKVLSYISV
 .*****.*.* * **.***.*.* **.*...**.***.***.* **.* *
 CG NAVAVTFSERLLGNFSLAVPIFVALSCFGSMNGGVFAVSRLFYVASREGHLPEILSMIHV

 5 HP RRLTPAPAIIFYGIIATIIYIIPGDINSLVNYFSFAAWLFYGLTILGLIVMRFRKELERP
 *. ** *.* * .. * ...**.***.*...*** **.***.* **.* **.* ...**
 CG RKHTPLPAVIVLHPLTMIMLFSGDLSLLNFLSFARWLFGLAVAGLIYLRYPDMHRP

 HP IKVPVVIPVLMTLISVFLVLAPIISKPTWEYLYCVLFILSGLLFYFLFVHY--KFGWAQK
 10 .****. **.*.....** .. **.***.* **.* . * * .
 CG FKVPLFIPALFSFTCLFMVALSLYSDP-FSTGIGFVITLTGVPAYYLFIIWDKKPRWFRI

 HP ISKPITMHLQMLMEVVPPEEDPE
 .*. **. **.*...**** *.
 15 CG MSEKITRTLQIILEVVPPEEDKL

The search of the GenBank using the base sequences
 of the present cDNA has revealed the registration of
 20 sequences that shared a homology of 90% or more (for example,
 Accession No. R07056) among ESTs. However, since they are
 partial sequences, it can not be judged whether or not they
 encode the same protein as the protein of the present
 invention.

25 <HP03612> (SEQ ID NOS: 34, 44 and 54)

Determination of the whole base sequence of the cDNA insert of clone HP03612 obtained from cDNA library of human kidney revealed the structure consisting of a 153-bp 5'-untranslated region, a 1128-bp ORF, and a 269-bp 3'-untranslated region. The ORF encodes a protein consisting of 375 amino acid residues and there existed seven putative transmembrane domains. Figure 14 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 39 kDa that was somewhat larger than the molecular weight of 37,930 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human monocarboxylate transporter (Accession No. AAC70919). Table 14 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human monocarboxylate transporter (MC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 41.7% in the N-terminal region of 192 amino acid residues.

Table 14

	HP	MTPQPAGPPDGGWGWVAAAAFAINGLSYGLLRSLGLAFPDLAEHFDRSAQDTAW
		.*. *****.*..*.* *.**.. * *. . .**
5	MC	MPPMPSAPPVHPPPDGGWGWIVVGATFISIGFSYAFPKAVTVFFKEIQQIFHTTYSEIAW
	HP	ISALALAVQQAASPVGSALSTRWGARPVVMVGGVLASLGFVFSAFASGLLHLYLGLGLLA
		.. * *.**.*.* ...*.****.***.* **.*...*.**....****.*...
	MC	ISSIMLAVMYAGGPVSSVLVNKYGSRPVVIAGLLCCLGMVLASFSSSVVQLYLTMGFIT
10	HP	GFGWALVFAPALGTLSTRYFSRRRVLAVGLALTGNGASSLLLAPALQLLLDTFGWRGALLL
		..*.**.*.*.* **..** . *** * *..****.*..*
	MC	GLGLAFNLQPALTIIGKYFYRKRPMANGLAMAGNPVFLSSLAPFNQYLFNTFGWKGSFLI
15	HP	LGAITLHLTPCGALLLPLVLPGDPPAPPRSPLAALGLSLFTRRAFSIFALGTALVGGGYF
		.. *. *. **
	MC	LGSLLLNA CVAGSLMRPLGPNQTTSKSKNKTGKTEDDSSPKKIKTKKSTWEKVNKYLD FS
	HP	VPYVHLAPRFRPGPGGIRSSAGGGRGCDGGCGRPAGLRVAGRPRLGAPPAAAGRIRGSDW
20	MC	LFKHRGFLIYLSGNVIMFLGFFAPIIFPAPYAKDQGIDEYSAAFLLSVMAFVDMFARPSV
	HP	AGAVGGGAGARGRRRELGGSPAGRGCLWAERGELRPAGFRCTPRAGGRRRCGAGHRAG
25	MC	GLIANSKYIRPRIQYFFSF AIMFNGVCHLLCPLAQDYTSVLVYAVFFGLGFGSVSSVLFE

HP DDADEPRGAPGPSVRLPKG

MC TLMDLVGAPRFSSAVGLVTIVECGPVLLGPPLAGKLVDLTGEYKMYMSCGAIVVAASVW

5

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI742291) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10407> (SEQ ID NOS: 35, 45 and 55)

15 Determination of the whole base sequence of the cDNA insert of clone HP10407 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 100-bp 5'-untranslated region, a 1053-bp ORF, and a 332-bp 3'-untranslated region. The ORF encodes a protein consisting of 350 amino acid residues and there existed at least four putative transmembrane domains. Figure 15 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

25 The search of the protein database using the amino acid sequence of the present protein revealed that: the

protein was longer by 35 amino acid residues at the N-terminus than human hypothetical protein (Accession No. CAB43375).

Furthermore, the search of the GenBank using the
5 base sequences of the present cDNA has revealed the registration of a clone beginning from the 117th base of the present cDNA (Accession No. AL050274).

<HP10713> (SEQ ID NOS: 36, 46 and 56)

Determination of the whole base sequence of the
10 cDNA insert of clone HP10713 obtained from cDNA library of human kidney revealed the structure consisting of a 79-bp 5'-untranslated region, a 2004-bp ORF, and a 611-bp 3'-untranslated region. The ORF encodes a protein consisting of 667 amino acid residues and there existed nine putative
15 transmembrane domains. Figure 16 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

20 The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse retinoic acid-responsive protein (Accession No. AAC16016). Table 15 shows the comparison between amino acid sequences of the human protein
25 of the present invention (HP) and mouse retinoic acid-

Table 15

10 HP MSSQPAGNQTS PGATEDYSYGSWYIDEPQGG EELQPEGEVPSCHT SIPPGLYHACLAS
*.***.*.*.*** *****.** *.**.****** . * * . **.* ****
MM MESQASENGSQTSSGVTDDYS--SWYIEEPLGAEEVQPEGVIPLCQLTAPPALLHACLAS

HP LSILVLLLLAMLVRRRQLWPDCVRGRPLSPVDFLAGDRPRAVPAAVFMVLLSSLCLLL

15 **.*****,*****.*** * . ***** .. *****,**. *.*****
MM LSFLVLLLLALLVRRRLWPRCGHRGLGLSPVDFLAGDLSWTVPAAVFVVLFSNLCLLL

HP PDEDALPFLT LASAPSQDGKTEAPRGAWKILGLFYAALYYPLAACATAGHTAAHL LGST
.**. *..*.*.**, *..**, **, *.*, **, *****, *** ** ***,.

20 MM PDENPLPFLNLT AASSPDGEMETSRGPWKLLALLYYPALYYPLAACASAGHQAAFLLGT V
HP LSWAHLGVQVWQRAEC PQVPKIYKYSSLASLPLLGLGFLSLWYPVQLVRSFSRRTGAG
*****,*****,***** *****.*****.*****.*****.*****.*****.
MM LSWAHFGVQVWQKAEC PQDPKIYKHYSLLASLPLLGLGFLSLWYPVQLVQSLRHRTGAG

25

- HP SKGLQSSYSEEYLRNLLCRKKLGSSYH-TSKHGFLSWARVCLRHCIYTPQPGFHLPLKLV
*.***.***.***.***.***.*.*.***...***.*..*.*****.*****
MM SQGLQTSYSEKYLRTLLCPKKLDSCSHPAKRSLLSRAWAFSHHSIYTPQPGFRLPLKLV
- 5 HP LSATLTGTAIYQVALLLLVGVVPTIQKVRAGVTTDVSYLLAGFGIVLSEDKQEVVELVKH
.*****.*****.****.*****.*****.*****.*****
MM ISATLTGTATYQVALLLLVSVVPTVQKVRAGINTDVSYLLAGFGIVLSEDRQEVVELVKH
- HP HLWALEVCYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAI
10 ***.*.***** ****.*.*** ***.***.*****.*.*.*****
MM HLWTVEACYISALVLSCASTFLLLIRSLRTHRANLQALHRGAALDLDPPLQSIHPSRQAI
- HP FCWMSFSAYQTAFICLGLLVQQIIFFLGTTALAFLVLMFVLHGRNLLLFRSLESSWPFWL
.****.***** *****.*****.*****.*.*****.*****.*****
15 MM VSWMSFCAYQTAFSCLGLLVQQVIFFLGTTSLAFLVFVPLLHGRNLLLRSLESTWPFWL
- HP TLALAVILQNMAAHVWFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSA
*.*****.***.*.*** **.*.*.*****.*.*****.*.*****.*.
MM TVALAVILQNIAANWIFLRTHHGYPELTNRRMLCVATFLLFPINMLVGAIMAVWRVLISS
20
- HP LYNAIHLGQMDLSLLPPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLPR
.**.***.*****.***.***.***.*****...***.***.*.* **
MM LYNTVHLGQMDLSLLPQRAASLDPGYHTYQNFLRIEASQSHPGVIAFCALLLHAPSPQPR
- 25 HP TMAAPQDSL RPGEDEGMQLLQTKDSMAKGARPGASRGARWGLAYTLLHNPTLQVFRKT

*****. **. ***** ***** . *. *****. **. ***.
 MM PPLAPQDSLRLPAEEEEGMQLLQTKDLMAKGAGHKGSQSRARWGLAYTLLHNPSLQAFRKA

HP ALLGANGAQP

5 ** .*. .
 MM ALTSAKANGTQP

The search of the GenBank using the base sequences
 10 of the present cDNA has revealed the registration of
 sequences that shared a homology of 90% or more (for example,
 Accession No. AI760170) among ESTs. However, since they are
 partial sequences, it can not be judged whether or not they
 encode the same protein as the protein of the present
 15 invention.

<HP10714> (SEQ ID NOS: 37, 47 and 57)

Determination of the whole base sequence of the
 cDNA insert of clone HP10714 obtained from cDNA library of
 human umbilical cord blood revealed the structure consisting
 20 of a 82-bp 5'-untranslated region, a 1395-bp ORF, and a
 1820-bp 3'-untranslated region. The ORF encodes a protein
 consisting of 464 amino acid residues and there existed a
 putative secretory signal at the N-terminus. Figure 17
 depicts the hydrophobicity/hydrophilicity profile, obtained
 25 by the Kyte-Doolittle method, of the present protein. In

vitro translation resulted in formation of a translation product of 49 kDa that was somewhat smaller than the molecular weight of 52,340 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 52 kDa. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Ala-Thr at position 164 and Asn-Asp-Ser at position 320). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from threonine at position 22.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA861134) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10716> (SEQ ID NOS: 38, 48 and 58)

Determination of the whole base sequence of the cDNA insert of clone HP10716 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 60-bp 5'-untranslated region, a 1413-bp ORF, and a 653-bp 3'-untranslated region. The ORF encodes a protein consisting of 470 amino acid residues and there existed one

putative transmembrane domain at the N-terminus. Figure 18 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 61 kDa that was larger than the molecular weight of 52,086 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human hypothetical protein CGI-90 (Accession No. AAD34085). Table 16 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human hypothetical protein CGI-90 (CG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 32.4% in the entire region.

Table 16

HP MSRLGALGGARAGLGLLLGTAAGLGFLCLLYSQRWKRTQRHGRSQSLPNSLDYTQTSDPG

HP RHVMLLRVPGGAGDASVLPSPREGQEKVLDRLDFVLTSLVALRREVEELRSSLRGLAG

25

HP EIVGEVRCHMEENQRVARRRRFPFVRERSDSTGSSSVYFTASSGATFTDAESEGGYTAN

CG MALAARLWRLLPFRRGAAPGSRLPA

5 HP AESDNERDSKESEDGEDEVSCETVKMGRKDSLDEEEAASGASSALEAGSSGLEDVLP

. * . . . *

CG GPSGSRGIAAPARFRGFVGMGNPGTFNRGLLSALSYLGFETYQVISQAAVHATAKVEE

HP LLQQADELHRGDEQKGREGFQLLNKL VYGSRQDFLWRLARAYSDMCELT-EEVSEKKS

10 . * . *** * . . * . * . *** . * ***** . * . * . . . ***

CG ILEQADYLYESGETEK--LYQLLTQYK--ESEDAELLWRLARASRDVAQLSRTSEEEKKL

HP YALDGKEEAEEALEKGDESADCHLWYAVLCGQLAEHESIQRRIQSGFSFKEHVDKAIALQ

. . . * * . ***** . . * * * * . * . * * * . * .

15 CG LVYEALEYAKRALEKNESFASHKWYAICLSDVGDYEGIKAKIANAYIIKEHFEKAIELN

HP PENPMAHFLLGRWCYQVSHLSWLEKKTATALLESPLSATVEDALQSFLKAEELQPGFSKA

. * . . . * . * * * * * . . . * . * . * . * * * * * * . * . . . * . * .

CG PKDATSIHLMGIWCYTFAEMPWYQRRIAKMLFATPPSSSTYEKALGYFHRAEQVDPNFYSK

20

HP GRVYISKCYRELGKNSEARWWWKLALCLPDVTKEDLAIQKDLEELEVLIRD

. . . . * * . * . . * . * . * . * . * . * * . * . . . *

CG NLLLLGKTYLKLHNKKLAALFWLMKAKDYPAHTEEDKQIQTEAAQLLTSFSEKN

25

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA852295) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10717> (SEQ ID NOS: 39, 49 and 59)

Determination of the whole base sequence of the cDNA insert of clone HP10717 obtained from cDNA library of human kidney revealed the structure consisting of a 73-bp 5'-untranslated region, a 732-bp ORF, and a 976-bp 3'-untranslated region. The ORF encodes a protein consisting of 243 amino acid residues and there existed two putative transmembrane domains. Figure 19 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36 kDa that was larger than the molecular weight of 26,270 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI478174) among ESTs. However, since they are partial sequences, it can not be judged whether or not they

encode the same protein as the protein of the present invention.

<HP10718> (SEQ ID NOS: 40, 50 and 60)

Determination of the whole base sequence of the
5 cDNA insert of clone HP10718 obtained from cDNA library of
human umbilical cord blood revealed the structure consisting
of a 86-bp 5'-untranslated region, a 813-bp ORF, and a 889-
bp 3'-untranslated region. The ORF encodes a protein
consisting of 270 amino acid residues and there existed
10 three putative transmembrane domains. Figure 20 depicts the
hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of 28 kDa that was smaller than the molecular weight of
15 31,116 predicted from the ORF.

The search of the protein database using the amino
acid sequence of the present protein revealed that the
protein was similar to *Caenorhabditis elegans* hypothetical
protein Y53C10A (Accession No. CAA22139). Table 17 shows the
20 comparison between amino acid sequences of the human protein
of the present invention (HP) and *Caenorhabditis elegans*
hypothetical protein Y53C10A (CE). Therein, the marks of -,
*, and . represent a gap, an amino acid residue identical
with that of the protein of the present invention, and an
25 amino acid residue similar to that of the protein of the

present invention, respectively. The both proteins shared a homology of 54.8% in the entire region other than the N-terminal region.

5 Table 17

	HP	MAGAEDWPGQ
	CE MTSSSAASSSTTTSSSTMPDENECLKKEERFKSPDPAPTLDEEVDIDTLPSMLEDDPNG	
10	HP QLELDEDEASCCRWGAQHAGARELAALYSPGKRLQEWCSVILCFSLIAHNLVHLLLLARW	
	.**.***.**.***** *.. . *.. ... ***. *	
	CE NVVECDLGFKGPRWGPQHAGAKKLASMYSKEKRLQEKVSLFAAIFLFSIVFIN-LLLS-W	
15	HP EDT--PLVILGVVAGALIADFLSGLVHWGADTWGSVELPIVGKAFIRPFREHHIDPTAIT	
	*.. *...* * ..***.*****.***.***** . *..*****.*****	
	CE ESSIWVSVLVSALVIMTADFASGLVHWAADTFGSVE-TWFGRSFIRPFREHHVDPTAIT	
	HP RHDFIETNGDNCLVTLLPLLNMAYKFRTHSPEALEQ--LYPWECFVFCIIIFGTFTNQIH	
20	***..*.*****. . ***. *. *. *. *. *. * ..** *. ..*****	
	CE RHDIVEVNGDNCMLCVGPLLWILYQQMTYQRDAITQWATFW--YILLGLIYVALTNQIH	
	HP KWSHTYFGLPRWVTLLQDWHVILPRKHHRIHHVSPHETYFCITTGWLNYPLEKIGFWRRL	
	***** **..**.*.*****.***.***.***.***.***.*****.***.*****.	
25	CE KWSHTYFGLPTWVFLQKAHIIILPRSHHKIHHISPHACYYCITTGWLNPLEYIGFWRKM	

HP EDLIQGLTGEKPRADDMKWAQKIK

* . . . ** . ** . ** . *** * . .

CE EWVVTTVTGMQPREDDLKWATKLQ

5

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA176107) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention. In addition, the region from position 466 to position 778 of the cDNA of the present invention matched with the region from position 2 to position 314 of human ubiquitin-conjugating enzyme E2 variant 1 (Accession NO. NM_003349) although no match was observed in another region.

20

<HP03745> (SEQ ID NOS: 61, 71 and 81)

25

Determination of the whole base sequence of the cDNA insert of clone HP03745 obtained from cDNA library of human kidney revealed the structure consisting of a 99-bp 5'-untranslated region, a 1170-bp ORF, and a 107-bp 3'-untranslated region. The ORF encodes a protein consisting of 389 amino acid residues and there existed at least nine

putative transmembrane domains. Figure 21 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human solute carrier family 7 (Accession No. NP_003974). Table 18 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human solute carrier family 7 (SC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 36.0% in the N-terminal region of 397 amino acid residues.

Table 18

20

HP	MDRGEKIQLKRVFGYWWGTSFLLINIIG
	..*..***. . . . *..*..* **
SC	MEAREPGRPTPTYHLVPNTSQSQVEEDVSSPPQRSSETMQLKKEISLLNGVSLVVGNMIG
HP	AGIFVSPKGVLAYSCMNVGVS LCVWAGCAILAMTSTLCSAEISISFPCSGAQYYFLKRYF

25

*****... . ** ***** **..... *** * .. *

SC SGIFVSPKGVLVHT-ASYGMSLIVWAIGGLFSVVGALCYAELGTTITKSGASYAYILEAF

HP GSTVAFLNLWTSFLGSGVVAG-QALLAEYSIQPFFPSCSVPKLPKKCLALAMLWIVGI

5 * . ** . ** . ** * . * . * *** ***** . * * . . * * *

SC GGFIAFIRLWVSLLVVEPTGQAIITFANYIIQPSFPSCDPPYLACRLLAAACICLLTF

HP LTRGVKEVTWLQIASSVLKVSILSFISLTGVVFLIRGKKENVERFQNAFDAELPDISHL

 . . . ** * . * . . ** * * . * . * * * . * . ** . ** . . . * . . . *

10 SC VNCAYVKWGTRVQDTFTYAKVVALIAIIVMGLVKLCQG—HSEHFQDAFEGSSWDMGNL

HP IQAIFQGYFAYSG—————ELKKPRTTIPKCIFTALPLVTVVYLLVNISYLTVLTPR

 * . . * . *** * . * . * * * . . . * . ** . * . * . * . * * . . . *

SC SLALYSALFSYSGWDTLNFVTEEIKNPERNLPLAIGISMPIVTLIYILTNAVYYTVLNIS

15 HP EILSSDAVAITWADRAFPSLAWIMPFAISTSLFSNLLISIFKSSRPIYLASQEGQLPLLF

 . . . ***** . * . ** . * . . * . . * . . * * . . * *** *** * . ** . ** *

SC DVLSSDAVAITFADQTFGMFSWTIPIAVALSCFGGLNASIFASSRLFFVGSREGHLPDLL

20 HP NTLNSHS-SPFTAVLLLVTGLSLAIILTSIDLINIFYFTGSLWSILLMIGILRRRYQEP

 * . * . * . * * ***** . * . . . * * . . * * . . **

SC SMIHIERFTPIPALFNCTMALIYLVIEDVFQLINIFYFSYWFFVGLSVVGQLYLRWKEP

HP NLSIPYKVKLDF

25 * * *

SC KRPRPLKLSVFFPIVFCICSVFLVIVPLFTDTINSLIGIGIALSGVPFYFMGVYLPESRR

<HP03747> (SEQ ID NOS: 62, 72 and 82)

5 Determination of the whole base sequence of the
cDNA insert of clone HP03747 obtained from cDNA library of
human umbilical cord blood revealed the structure consisting
of a 21-bp 5'-untranslated region, a 1047-bp ORF, and a
1324-bp 3'-untranslated region. The ORF encodes a protein
10 consisting of 348 amino acid residues and there existed a
putative secretory signal at the N-terminus and one putative
transmembrane domain at the C-terminus. Figure 22 depicts
the hydrophobicity/hydrophilicity profile, obtained by the
Kyte-Doolittle method, of the present protein. In vitro
15 translation resulted in formation of a translation product
of 40 kDa that was almost identical with the molecular
weight of 39,685 predicted from the ORF. Application of the
(-3,-1) rule, a method for predicting the cleavage site of
the secretory signal sequence, allows to expect that the
20 mature protein starts from proline at position 39.

 The search of the protein database using the amino
acid sequence of the present protein revealed that the
protein was similar to human endoplasmic reticulum
glycoprotein (Accession No. NP_006807). Table 19 shows the
25 comparison between amino acid sequences of the human protein

10

*. * ****. .. *. * **** **. *.**

***** ***** . * . ** . * . * . ** . ***** . ** . * . ** . ***** . ***** .

*****.*****.***.***.*** ** .*****. ** . .*.*.*.*.*

BNSDOCID: <WO 0112660A2 I >

HP EWRDCIEVPGVRLPRGYFGTSSITGDLSDNHDVISLKL FELTVERTPEEEKLHRDVF LP

...** ***, *****, * **, **, ***... . *

ER EWKNCIDITGVRLPTGYFYGASAGTGDLSNDHDIISMKLFQLMVEHTPDEESIDWTKIEP

5

HP SVDNMKLP-----EMTAPL--PPLSGLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRK

*** ** , * . *** ,**... *. * **...*,**.. *

ER SVNFLKSPKDNVDDPTGNFRSGPLTGWRVFLLLCALLGIVVCAVVGAVVFQKRQERN-K

10 HP RFY

ER RFY

15 Furthermore, the search of the GenBank using the
base sequences of the present cDNA has revealed the
registration of sequences that shared a homology of 90% or
more (for example, Accession No. AA262924) among ESTs.
However, since they are partial sequences, it can not be
20 judged whether or not they encode the same protein as the
protein of the present invention.

<HP10719> (SEQ ID NOS: 63, 73 and 83)

Determination of the whole base sequence of the
cDNA insert of clone HP10719 obtained from cDNA library of
human kidney revealed the structure consisting of a 54-bp

5'-untranslated region, a 786-bp ORF, and a 576-bp 3'-untranslated region. The ORF encodes a protein consisting of 261 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 23 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 33 kDa that was larger than the molecular weight of 27,435 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from asparagine at position 19.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mouse endomucin (Accession No. AAD05208). Table 20 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mouse endomucin (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 47.9% in the entire region.

25

Table 20

	HP	MELLQVTIL-FLLP-SIC-SSNSTGVL-EAANNSLVVTTTKPSITTPNTESLQKNVVTPT
		* ***,*. * ***, *. * *.* ***,*. *. *. *. * .. *
5	MM	MRLQATVLFLLSNSLCHSEDGKDVQNDSIPTAETSTTKASVTIPGIVSV-TNPKNKA
	HP	TGTPPGTITNELLKMSLMSTATFLTskDEGLKATTTDVRKNDSIISNVTVTSVTLPNAV
		.. ***,*. ***, *. * *. ***, *. * *. ***, **
	MM	DGTPPEGTTKSDVSQTSLVTTINSLTTPKHEVGTTTEGPLRNESSTMKITVPNTPTSNAN
10	HP	STLQSSPKTETQSSIKTTEIPGSVLQPDASPKTGTLSIPVTIPENTSQSQVIGTEGG
		***, *. *. ** *. ** * .. **.
	MM	STLPGSQNKITTQ-----LLDALPKITATPS-----ASLTTAHTMSLLQDTEDR
15	HP	KNASTSATSRSYSSIILPVVIALIVITLSVFVLVGLYRMCWKADPGTPENGNDQPQSDKE
		* *. *. *. *. *****. ***** ***, *****. *** *****
	MM	KIATTPSTTPSYSSIILPVVIALVVITLLVFTLVGLYRICWKRPDGPENGNDQPQSDKE
	HP	SVKLLTVKTISHESGEHSAQGKTKN
20		*****
	MM	SVKLLTVKTISHESGEHSAQGKTKN

The search of the GenBank using the base sequences
 25 of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. AA486620) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10720> (SEQ ID NOS: 64, 74 and 84)

Determination of the whole base sequence of the cDNA insert of clone HP10720 obtained from cDNA library of human kidney revealed the structure consisting of a 25-bp 5'-untranslated region, a 669-bp ORF, and a 653-bp 3'-untranslated region. The ORF encodes a protein consisting of 222 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 24 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 28 kDa that was somewhat larger than the molecular weight of 25,219 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 35 kDa. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Val-Thr at position 76 and Asn-His-Thr at position 93). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to

expect that the mature protein starts from glutamic acid at position 15.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792241) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10 <HP10721> (SEQ ID NOS: 65, 75 and 85)

Determination of the whole base sequence of the cDNA insert of clone HP10721 obtained from cDNA library of human kidney revealed the structure consisting of a 74-bp 5'-untranslated region, a 552-bp ORF, and a 1658-bp 3'-untranslated region. The ORF encodes a protein consisting of 183 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 25 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 23 kDa that was somewhat larger than the molecular weight of 19,989 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 22 kDa. Application of the (-3,-1) rule, a method for predicting the

15

20

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cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamic acid at position 25.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R27187) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10725> (SEQ ID NOS: 66, 76 and 86)

Determination of the whole base sequence of the cDNA insert of clone HP10725 obtained from cDNA library of human kidney revealed the structure consisting of a 235-bp 5'-untranslated region, a 789-bp ORF, and a 713-bp 3'-untranslated region. The ORF encodes a protein consisting of 262 amino acid residues and there existed one putative transmembrane domain. Figure 26 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example,

Accession No. AI127782) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

5 <HP10727> (SEQ ID NOS: 67, 77 and 87)

Determination of the whole base sequence of the cDNA insert of clone HP10727 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 102-bp 5'-untranslated region, a 507-bp ORF, and a 947-
10 bp 3'-untranslated region. The ORF encodes a protein consisting of 168 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 27 depicts the hydrophobicity/hydrophilicity profile, obtained by the
15 Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 24 kDa that was larger than the molecular weight of 17,822 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 23 kDa.
20 Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from lysine at position 29.

The search of the GenBank using the base sequences
25 of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. R80316) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10728> (SEQ ID NOS: 68, 78 and 88)

Determination of the whole base sequence of the cDNA insert of clone HP10728 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 221-bp 5'-untranslated region, a 732-bp ORF, and a 902-bp 3'-untranslated region. The ORF encodes a protein consisting of 243 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 28 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was larger than the molecular weight of 26,534 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H23535) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10730> (SEQ ID NOS: 69, 79 and 89)

Determination of the whole base sequence of the cDNA insert of clone HP10730 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 27-bp 5'-untranslated region, a 1287-bp ORF, and a 1216-bp 3'-untranslated region. The ORF encodes a protein consisting of 428 amino acid residues and there existed one putative transmembrane domain. Figure 29 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 50 kDa that was somewhat larger than the molecular weight of 48,992 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. C19105) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10742> (SEQ ID NOS: 70, 80 and 90)

Determination of the whole base sequence of the cDNA insert of clone HP10742 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 231-bp 5'-untranslated region, a 852-bp ORF, and a 828-

bp 3'-untranslated region. The ORF encodes a protein consisting of 283 amino acid residues and there existed two putative transmembrane domains. Figure 30 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was smaller than the molecular weight of 31,629 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T35949) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03800> (SEQ ID NOS: 91, 101 and 111)

Determination of the whole base sequence of the cDNA insert of clone HP03800 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 67-bp 5'-untranslated region, a 1431-bp ORF, and a 135-bp 3'-untranslated region. The ORF encodes a protein consisting of 476 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 31 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In

vitro translation resulted in formation of a translation product of 55 kDa that was almost identical with the molecular weight of 54,110 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 58 kDa. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Lys-Thr at position 81, Asn-Met-Thr at position 132, Asn-Val-Thr at position 307 and Asn-Gln-Thr at position 346). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 23.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to mosquito vitellogenic carboxypeptidase (Accession No. P42660). Table 21 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and mosquito vitellogenic carboxypeptidase (VC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 44.5% in the entire region. In addition, the C-terminal portion beginning from alanine at position 182 matched with

human probable carboxypeptidase (Accession No. AAC23787)
except one amino acid residue.

Table 21

5

HP MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPK-GDSGQPLFLTPYIEAGKIQKG

... * * . ** . *.**.*.....*.....

VC MVKFHLLVLI AFTCYTCS DATLWNPYKKLMRGSASPPRPGESGEPLFLTPLLQDGKIEEA

10

HP RELSLVGPFPG LNMKSYAGFLT VNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSM

* . . * ** . ** . ** ** * . ** ** .

VC RNKARVNHPMLSSVESYSGFMTVDAKHNSNLFFWYVPAKNNREQAPILVWLQGGPGASSL

HP FGLFVEHGPYVVT SNMTLRDRDFPWTTL SMLYIDNPVGTGFSFTDDTHGYAVNEDDVAR

15

** . * * . ** . . . * * . . . * . . . * .

VC FGMFEENGPFHHRNKS VKQREYSWHQNHI MIYIDNPVGTGFSFTDSDEGYSTNEEHVGE

HP DLYSALIQQFFQIFPEYKNND FYVTGESYAGKYVPAIAHLIHS LNPVREV KINLNGIAIGD

. * ** . ** ** ** . ** ** . * ** .

20

VC NLMKFIQQFFVLFPNLLKHPFYISGESYGGKFVPAFGYAIH-NSQS QPKINLQGLAIGD

HP GYSDPESIIGGYAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGD

** . ** * . * . ** . ** . * . . . * * * * . **

VC GYTDPLNQL-NYGEYLYELGLIDLNGRKKFDEDTAAAIACAERKDMNSANRLIQGLFDG-

25

HP LTSDPSYFQNVGTGCSNYYNFLRC-TEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVE

*... ***...*** *.****...*.***...***...***...*.***...

VC LDGQESYFKKVTGFSSYYNFIKDEESKQDSVLMFSLNPEVRKGIHVGELPFHDSGDGHN

5 HP K---YLREDTVQSVKPWLTEIMNNYKVLINQQLDIIVAAALTEHSLMGMDWKGSQEYKK

* *.***...* **.....*.**.*.....*...*...*...*...*...*

VC KVAEMLSEDTLDTVAPVWSKLLSHYRVLFYNGQLDIICAYPMTVDFLMKMPFDGDSEYKR

HP AEKKVWKIFKSDSEVAGYIRQAGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGWDP

10 *... *..*.***...**...*.***...*.***...***...***...*

VC ANRE---IYRVDGEIAGYKKRAGRLQEVLI RNAGHMVPRDQPKWAFDMITSFTHKNYL

HP YVG

15

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA095665) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03831> (SEQ ID NOS: 92, 102 and 112)

25 Determination of the whole base sequence of the cDNA insert of clone HP03831 obtained from cDNA library of

human kidney revealed the structure consisting of a 191-bp 5'-untranslated region, a 681-bp ORF, and a 223-bp 3'-untranslated region. The ORF encodes a protein consisting of 226 amino acid residues and there existed four putative transmembrane domains. Figure 32 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human claudin-10 (Accession No. NP_008915). Table 22 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human claudin-10 (CD). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 76.2% in the entire region. The C-terminal region downstream from glycine at position 72 completely matched with that sequence.

Table 22

. . * * . . . * *** * . . . *** ** . * . . . *

CD MASTASEIIAFMVISISGWLVSSLTPTDYWKVSTIDGTVITTATYWANLWKACVTDSTGV

5 HP FHCPRHFTIFKVAGYIQACRGLMIAAVSLGFFGSIFALFGMKCTKVGGSDKAKAKIACLA

```
*****
```

CD SNCKDFPSMLALDGYIQACRGLMIAAVSLGFFGSIFALFGMKCTKVGGSDKAKAKIACLA

HP GIVFILSGLCSMTGCSLYANKITTEFFDPLFVEQKYELGAALFIGWAGASLCIIGGVIFC

10 *****

CD GIVFILSGLCSMTGCSLYANKITTEFFDPLFVEQKYELGAALFIGWAGASLCIIGGVIFC

HP FSISDNNKTPRYTYNGATSVMSRKYHGGEDFKTTNPSKQFDKNAYV

15 CD FSISDNNKTPRYTYNGATSVMSRKYHGGEDFKTTNPSKQFDKNAYV

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N41613) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

25. <HP03879> (SEQ ID NOS: 93, 103 and 113) --

Determination of the whole base sequence of the cDNA insert of clone HP03879 obtained from cDNA library of human kidney revealed the structure consisting of a 33-bp 5'-untranslated region, a 918-bp ORF, and a 651-bp 3'-untranslated region. The ORF encodes a protein consisting of 305 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 33 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 34 kDa that was almost identical with the molecular weight of 34,073 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human NADH-cytochrome b5 reductase (Accession No. Y09501). Table 23 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human NADH-cytochrome b5 reductase (CT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 63.5% in the entire region other than the N-terminal region.

Table 23

	HP	MGIQTSPVLLASLGVGLVTLLGLAVGSYLVRRSRPQVTLLDPNEKYLLRLLDKTTVSHN	
		* . ** * . ** . * . ** **** . * . . . ** .	
5	CT	MGAQLSTLGHMVLFPVWFLYSLLMKLFQRS-TPAITLESPDIKYPLRLIDREIISHD	
	HP	TKRFRFALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQGYVDLVIKVYLKG	
		* . ***** . . . * . ***** . ***** . ***** . ** . ***** . ** . * . * . ***** . *	
	CT	TRRFRFALPSPQHILGLPVGQHIYLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKD	
10	HP	VHPKFPEGGKMSQYLDCLKVGDVVEFRGPSGLLTYTGKGFNIQPNKKSPPPEPRVAKKLG	
		. ***** . ***** . * . . ** . ***** . * **** . * . * . * . * . * . * . *	
	CT	THPKFPAGGKMSQYLESMQIGDTIEFRGPSGLLVYQKGKFAIRPDKKSNIIRTVKSVG	
15	HP	MIAGGTGITPMLQLIRAILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFLKW	
		***** . ***** . * . * . * . * . * . * . * . * . * . * . * . * . *	
	CT	MIAGGTGITPMLQVIRAIMKDPDDHTVCHLLFANQTEKDILLRPELEELRNKHSARFKLW	
	HP	FTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMVQLACHPNLDKLGYSQK	
20		. *** . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *	
	CT	YTLDRAPEAWDYGGGFVNEEMIRDHLPPPEEEPLVLMCGPPPMIQYACLPNLDHVGHPT	
	HP	MRFTY	
		* . .	
25	CT	RCFVF	

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. F06459) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

10 <HP03880> (SEQ ID NOS: 94, 104 and 114)

Determination of the whole base sequence of the cDNA insert of clone HP03880 obtained from cDNA library of human kidney revealed the structure consisting of a 98-bp 5'-untranslated region, a 684-bp ORF, and a 115-bp 3'-untranslated region. The ORF encodes a protein consisting of 227 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 34 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 28 kDa that was somewhat larger than the molecular weight of 25,717 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 27 kDa. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to

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expect that the mature protein starts from aspartic acid at position 23.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to rat phosphatidylethanolamine-binding protein (Accession No. P31044). Table 24 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and rat phosphatidylethanolamine-binding protein (RN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 37.6% in the region of 133 amino acid residues other than the N-terminal region.

Table 24

	HP	MCWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKV
20		
	RN	MAADISQWAGPLSLQEVDEPPQHALRVDYGGVTV
	HP	VPDCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKG
	 * * *.**..***** .*. * *.**..**
25	RN	DELGKVLTPQTQVMNRPSSISWDGLDPGKLYTLVLTPDAPSRKDPKFREWHHFLVVMKGA

HP ADLKKGKIQQELSA YQAPSPPAHSGFHRYQFFVYLQEGKV---ISLLP-KENKTRGSWK

* * * * *

RN NDISSGTV----LSEYVGSGPPKDTGLHRYVWLVEEQEQPLNCDEPILSNKSGDNRGKFK

5

HP MDRFLNRFHLGEPEASTQFMTQNYQDSPTLQAPRERASEPKHKNQAEI AAC

.....*.....***.*.*.*.....*.*

RN VESFRKKYHLGAPVAGTCFQAEWDDSVPKLHDQLAGK

10

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H83784) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10704> (SEO ID NOS: 95, 105 and 115)

Determination of the whole base sequence of the
20 cDNA insert of clone HP10704 obtained from cDNA library of
human kidney revealed the structure consisting of a 141-bp
5'-untranslated region, a 1326-bp ORF, and a 399-bp 3'-
untranslated region. The ORF encodes a protein consisting of
441 amino acid residues and there existed eight putative
25 transmembrane domains. Figure 35 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

5 The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human unknown gene product (Accession No. AAC27544). Table 25 shows the comparison between amino acid sequences of the human protein of the present invention
10 (HP) and human unknown gene product (UP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins
15 shared a homology of 39.1% in the entire region.

Table 25

20	<p>HP MAIHKALVMCLGLPLFLFPG-AWAQGHVPPGCSQGLNPLYYNLCDRSGAWGIVLE</p> <p> * **.... ***..* * * ..**..* ..**..*</p> <p>UN MFVASERKMRAHQVLTFLLLFVITSVASENASTSRGCGDLLPQYVSLCDLDAIWGIVVE</p>
25	<p>HP AVAGAGIVTTFVLTIIIVASLPFVQDTKKRSLLGTQVFFLLGTLGLFCLVFACVVKPDFS</p> <p> ***** ..*..* ..**..**.....* * ..* ..***** *..** ..*..*</p> <p>UN AVAGAGALITLLMLIILVRLPFIKEKEKSPVGLHFLFLLGTLGLFGLTFAFIIQEDET</p>

HP TCASRRFLFGVLFAICFSCLAAHVFAFNFLARKNHGPRGWVIFTVALLTLVEVIINTEW

. *. ****. ****. ****. *. *. ** ** . . . ** * **. ***. **

UN. ICSVRRFLWGVLFAICFSCLLSQAWRVRLVRHGTGPAGWQLVGLALCLMLVQVIAVEW

5

HP LIITLVRGSGEGGPQGNSSAGWAVASPCAIANMDFVMALIYVMLLLLGAFLGAWPALCGR

*. *. *. ** . ***** *. **. . . * . ***.

UN LVLTVLR-----DT-----RPACAYEPMDFVMALIYDMVLLVVTGLGLALFTLCGK

10

HP YKRWRKHGVFVLLTTATSVAIWVWVIMTYGN-KQHNSPTWDDPTLAIALAANAWAFVL

. ***. *. *. *. *. ** ***. *. *. *. ** * . . . *. ****. ***. *. **.

UN FKRWKLNGAFLITAFSLVLIWVWMTMYLFGNVKLQQGDAWNPDLAITLAASGWVFI

HP FYVIPEVSQVTKSSPEQSYQGDMYPTRGVGY-ETILKEQ-KGQSMFVENKAFSMDEPVAA

15

*. ***. . * . . *. . . *. ** *****. **

UN FHAIPEI-HCTLLPALQENTPNYFDTSQPRMRETAFEEDVQLPRAYMENKAFSMDEHNAA

HP KRPVS-PYSGYNGQLLTSVYQPTMALMHKVPSEGAYDIILPRATANSQVMGSANSTLRA

*... * *. * * * *

20

UN LRTAGFPNGSLGKRPSGLGKRPSAPFRSNVYQPTMAVVLNGGTIPTAPPSHTGRHLW

HP EDMYSAQSHQAATPPKDGKNSQVFRNPYVWD

25

The search of the GenBank using the base sequences

of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA346702) among ESTs. However, since they are partial sequences, it can not be judged whether or not they
5 encode the same protein as the protein of the present invention.

<HP10715> (SEQ ID NOS: 96, 106 and 116)

Determination of the whole base sequence of the cDNA insert of clone HP10715 obtained from cDNA library of
10 human umbilical cord blood revealed the structure consisting of a 49-bp 5'-untranslated region, a 798-bp ORF, and a 1351-bp 3'-untranslated region. The ORF encodes a protein consisting of 265 amino acid residues and there existed two putative transmembrane domains. Figure 36 depicts the
15 hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 43 kDa that was larger than the molecular weight of 29,217 predicted from the ORF.

20 The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI381750) among ESTs. However, since they are partial sequences, it can not be judged whether or not they
25 encode the same protein as the protein of the present

invention.

<HP10724> (SEQ ID NOS: 97, 107 and 117)

Determination of the whole base sequence of the cDNA insert of clone HP10724 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 68-bp 5'-untranslated region, a 627-bp ORF, and a 1485-bp 3'-untranslated region. The ORF encodes a protein consisting of 208 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 37 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 24 kDa that was almost identical with the molecular weight of 23,850 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T78035) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10733> (SEQ ID NOS: 98, 108 and 118)

Determination of the whole base sequence of the cDNA insert of clone HP10733 obtained from cDNA library of human umbilical cord blood revealed the structure consisting

of a 102-bp 5'-untranslated region, a 1203-bp ORF, and a 222-bp 3'-untranslated region. The ORF encodes a protein consisting of 400 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the inner portion. Figure 38 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 50 kDa that was larger than the molecular weight of 43,151 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 54 kDa. In addition, there exist in the amino acid sequence of this protein four sites at which N-glycosylation may occur (Asn-Leu-Thr at position 52, Asn-Ala-Ser at position 131, Asn-Ile-Thr at position 145 and Asn-Leu-Ser at position 343). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from arginine at position 33.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Drosophila melanogaster* GOLIATH protein (Accession No. Q06003). Table 26 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Drosophila melanogaster*

GOLIATH protein (DM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 35.0% in the entire region.

Table 26

10 HP MAWRRREASVGARGVLALALLALALCVPGARGRALEWFSAVVNIEYVDPQTNLTWWSVSE

HP SGRFGDSSPKEGAHGLVGVPWAPGGDLEGCAPDTRFFVPEPGGGAAPWVALVARGGCTF

HP KDKVLVAARRNASAVVLYNEERYGNITLPM SHAGTGNIVVIMISYPKGREILEL-VQKGI

15 * *... ..*.*.. ..*.*..**

DM MQLEKMQIKGKTRNIAAVITYQNIGQDLSLTLDKGY

HP PVTMTIGVGTRHVQEF--ISGQSVVFVAIAFITMMIISLAWLIFYIYIQRFLY-TGSQIGS

..* * * *... ..**.*.*.* * .. *

20 DM NVTISIIIEGRRGVRTISSLNRTSVLFVSISFI--VDDILCWLIFYIYIQRFRYMQAKDQQS

HP QSHRKETKKVIGQLLLHTVKHGEKGIDVDAENCAVCIENFKVKDIIRILPCKHIFHRICI

..* *... ..*.*..**.*.*.*.*.*.*.*.***.*

DM RNLC SVTKKAIMKIPTKTGKFSD-EKDLDSDCCAICIEAYKPTDTIRILPCKHEFHKNCI

25

HP DPWLLDHRTCPMCKLDVIKALGYWGE PGDVQEMPAPESPPGRDPAANLSLALPDDGSD
 *****.* ** ... *. *.
 DM DPWLIHRTCPMCKLDVLKFGY-VVGDQIYQTPSPQHTAPIASIEEVPVIVVAVPHGPQ
 5 HP SSPPSASPAESEPQCDPSFKGDAGENTALLEAGRSDSRHGGPIS
 . . * . . . * . . . *
 DM PLQPLQASNMFAPSHYFQSSRSPSSSVQQQLAPLTYQPHPQQAASERGRNRNSAPATMP

10 The search of the GenBank using the base sequences
 of the present cDNA has revealed the registration of
 sequences that shared a homology of 90% or more (for example,
 Accession No. AI286184) among ESTs. However, since they are
 partial sequences, it can not be judged whether or not they
 15 encode the same protein as the protein of the present
 invention.

<HP10734> (SEQ ID NOS: 99, 109 and 119)

Determination of the whole base sequence of the
 cDNA insert of clone HP10734 obtained from cDNA library of
 20 human umbilical cord blood revealed the structure consisting
 of a 124-bp 5'-untranslated region, a 579-bp ORF, and a
 1202-bp 3'-untranslated region. The ORF encodes a protein
 consisting of 192 amino acid residues and there existed one
 putative transmembrane domain. Figure 39 depicts the
 25 hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human sodium channel $\beta 2$ subunit (Accession No. AAD47196). Table 27 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human sodium channel $\beta 2$ subunit (SC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 26.3% in the N-terminal region of 152 amino acid residues.

Table 27

20 HP MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQS--TEDK
 SC MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNH
 HP CIFKIDWTLSPGEHAKDE-YVLYYYNSLSVPIGRFQNRVHLMGDNLCNDGSLLLQDVQEA
 SC KQFSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMLRNVQPE

HP DQGTyceIRLKGESQVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVE

..*.*.*.**.*.*.*.

SC DEGIYNCYIMNPPDRHRGHGKIHLQVLMEEPPERDFTVAVIVGASVGGFLAVVILVMV

5

HP WIFSGRRRAKVTRRKHHCVREGSG

SC KCVRRKKEQKLSTDDLKTEEEGKTDGEGNPDDGAK

10

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. C03216) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10756> (SEQ ID NOS: 100, 110 and 120).

Determination of the whole base sequence of the cDNA insert of clone HP10756 obtained from cDNA library of human kidney revealed the structure consisting of a 49-bp 5'-untranslated region, a 783-bp ORF, and a 166-bp 3'-untranslated region. The ORF encodes a protein consisting of 260 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 40 depicts the

25

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was almost identical with the molecular weight of 27,356 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AW027769) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03670> (SEQ ID NOS: 121, 131 and 141)

Determination of the whole base sequence of the cDNA insert of clone HP03670 obtained from cDNA library of human umbilical cord blood revealed the structure consisting of a 77-bp 5'-untranslated region, a 1014-bp ORF, and a 531-bp 3'-untranslated region. The ORF encodes a protein consisting of 337 amino acid residues and there existed at least seven putative transmembrane domains. Figure 41 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to human hypothetical protein KIAA0260

(Accession No. BAA13390). Table 28 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and human hypothetical protein KIAA0260 (KI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 57.6% in the entire region other than the N-terminal region. In addition, the C-terminal region beginning from leucine at position 77 matched with human putative Sqv-7-like protein (Accession No. AJ005866) except one amino acid residue.

Table 28

15

HP MTAGGQAEAEAGAGGEPG

KI NSWSPLGAAAAGPRAARPRRQATAAAAAAMAEVHRRQHARVKGEAPAKSSTLRDEEELGMA

20

HP AARLPSRVARLLSALFYGTCSFLIVLVNKALLTTYGFPSIFLGIGQMAATIMILYVSKL

..**.****.*****.***.***.****.***.***.***.***.*

KI SAETLTVFLKLLAAGFYGVSSFLIVVVKSVLTNYRFPSSLCVGLGQMVA TVAVLWVGKA

HP NKIIHFPDFDKKIPVKLFPLPLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLETI

25

.....***.*...* * ***** **.* ** **.* *****.*.*.*.*..

KI LRVVKFPDLDRNVPRKTFPLPLLYFGNQITGLFSTKKLNLPMTVLRRFSILFTMFAEGV

HP ILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLNDIFTAANGVYTKQKMDPK

. * * . * . * . . * * * . * . * * * . * * . * * * * * . * . . * * . . * * * * . * . * . * . * . *

5 KI LLKKTFSWGIKMTVFAMIIGAFVAASSDLAFDLEGYAFILINDVLTAAANGAYVKQLDSK

HP ELGKYGVLFYNACFMIIPTLIISVSTGDLQQATEFNQWKNVVFILQFLSCFLGFLMYS

*****. *. ***** ***, ***** *. ***** *. *. ***** * . . *. ***** ***** ***, *****.

KI ELGKYGLLYNALFMILPTLAIAYFTGDAQKAVEFEGWADTLFLLQFTLSCVMGFILMYA

10

HP TVLCSYYNSALTTAVVGAIKNVSVAYIGILIGGDYIFSLNLFVGLNICMAGGLRYSFTL

*****. *****. ** ****. . . ****. . *****. ** *****. **.* ****. *

KI TVLCTQYNSALTTTIVGCIKNILITYIGMVFGGDYIFTWTNFIGLNSIAGSLVYSYITE

15 HP SSQLKPKPVGEENICLDLKS

... * * * ** *

KI TEEQLSKQ-SEANNKLDIKGKGAV

20 The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. R24922) among ESTs. However, since they are
partial sequences, it can not be judged whether or not they
25 encode the same protein as the protein of the present

invention.

<HP03688> (SEQ ID NOS: 122, 132 and 142)

Determination of the whole base sequence of the
cDNA insert of clone HP03688 obtained from cDNA library of
5 human umbilical cord blood revealed the structure consisting
of a 35-bp 5'-untranslated region, a 711-bp ORF, and a 1729-
bp 3'-untranslated region. The ORF encodes a protein
consisting of 236 amino acid residues and there existed five
putative transmembrane domains. Figure 42 depicts the
10 hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of high molecular weight.

The search of the protein database using the amino
15 acid sequence of the present protein revealed that the
protein was similar to *Caenorhabditis elegans* hypothetical
protein W02D9 (Accession No. CAB03470). Table 29 shows the
comparison between amino acid sequences of the human protein
of the present invention (HP) and *Caenorhabditis elegans*
20 hypothetical protein W02D9 (CE). Therein, the marks of -, *,
and . represent a gap, an amino acid residue identical with
that of the protein of the present invention, and an amino
acid residue similar to that of the protein of the present
invention, respectively. The both proteins shared a homology
25 of 50.8% in the entire region other than the N-terminal

region.

Table 29

5	HP	MAEAE
	CE	MEILNLSSKFSLSDKPCQKFIFSLFSVQNSRFKIISFPEIHQKPLPQEEMNSFGNASVD
	HP	SPGDPGTASPRPLFAGLSDISISQDIPVEGEITIPMRSRIREFDSSTLNESVRNTIMRDL
10		**.. . . **. *. *. *. *. *
	CE	IDMLEQEMAAEQTANLSGNIAGMSAPKSSSNRRGPMQEVDLDAEFDTLEEPVWDTVKRDV
	HP	KAVGKKFMHVLYPR-KSNTLLRDWDLWGPLILCVTLALMLQRDSADSEKDGGPQFAEVFV
		. ** ** *. * *****. **. ***. **. ***. **.
15	CE	LTVGAKFTHVVLPHGDKQLLRDWDWGLFICVGLALLQH---NGGTESAPQFTQVFT
	HP	IVWFGAVTITLNSKLLGGNISFFQSLCVLGYCILPLTVAMLICRLVLLADPGPVNFMVRL
		*. **. *. * * *****. ***. ** ** .. *. * . * . . * . **
	CE	ITFFGSVIVTANIKLLGGNISFFQSLCVIGYCLLPPFVAAVLCSL-FLHGI---AFPLRL
20		
	HP	FVVIVMFAWSIVASTAFLADSQPPNRRALAVYPVFLFYFVISWMILTFTPQ
	 *. **. ** . ***. ** .. * * . *****. ****.
	CE	LITSIGFVWSTYASMGFLAGCQPDKKRLVIYPVFLFYFVVSWMIISHS

25

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T51465) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03825> (SEQ ID NOS: 123, 133 and 143)

Determination of the whole base sequence of the cDNA insert of clone HP03825 obtained from cDNA library of human kidney revealed the structure consisting of a 20-bp 5'-untranslated region, a 1683-bp ORF, and a 36-bp 3'-untranslated region. The ORF encodes a protein consisting of 560 amino acid residues and there existed seven putative transmembrane domains. Figure 43 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 56 kDa that was smaller than the molecular weight of 64,047 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Mycobacterium tuberculosis* hypothetical protein Rv0235c (Accession No. CAB07001). Table 30 shows the comparison between amino acid sequences

of the human protein of the present invention (HP) and Mycobacterium tuberculosis hypothetical protein Rv0235c (MT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 41.7% in the entire region other than the N-terminal region. In addition, the region from alanine at position 293 to proline at position 502 matched with human putative novel protein c360B4.1 (Accession No. CAB56180).

Table 30

15	HP MAAPAESLRRRK TGYS DPEPES PPAPGR GPAGSPAHLHTGTFWLTRIVLLKALAFVYFVA	
		. . . **.*.* . . *.*.*
	MT	MGWFSAP EYWLGR LALERGTAI IYLIA
	HP FLVAFHQNKQLIGDRG L LPCR VFLKNFQQYFQDRTSWEVFSYMP TILW LMDWSDMNSNLD	
20	*.*.* . . ***.*.* . . *.* *.* *	
	MT FVAAAQQFRPLIGEHGMLPVPRYLAG-QSFWRTPSIFH-FRYS DRV FAGVCW--LGAVLS	
	HP LLALLGLGISSFVLITGCANMLLMAALWGLYMSLVNVGHVWYSFGWESQLLETGFLGIFL	
	* . * .*** . . *.** . . ** **.*.*****.***** ***** ***	
25	MT --AAVVAGAASFVPLW--ATMLIWLTLWVLYLSIVNVGQAWYSFGWESLLLETGFLMIFL	

HP CPLWTL SRLPQH TPTS RIVLWGFRWLIFRIMLGAGLIKIRGDRCDLTCMDFHYETQPM

. * . . * . * . *** ** . ***** . **** . **** . **** . * . *****

MT GNERT-----APPILTLA-RWLLFRVEFGAGLIKMRGDSWRSALTCLYYHHETQPM

5

HP PNPVAYYLHHSPWWFHRFETLSNHFIELLVPFFFLGRRACIIHGVLQILFQAVLIVSGN

..*.*.* ** * .***.*.***.*.**** ** . * * . . . * * .***

MT PGPLSWFFHHLPKPLHRIEVAGNHFAQLVVPFGLFTPQPAASIAAAIIVVTQLWLVASGN

10

HP LSFLNWLTMVPSLACFDDATLGFLFPSGPGSLKDRVLMQQRDIRGARPEPRFGSVVRRRAA

MT FSWLNWLTL--LAC---SAID--TSS-AAAL----LPMPAQALSAPPQWFAGLV---V

15

HP NVSLGVLLAWLSVPVVLNLLSSRQVMNTHFNSLHIVNTYGAFGSITKERAEVILQGTASS

..*** ** ..*****. * ** ***. *. ***** .. * **.. **.. *

MT VFTAAVLL--LSYWPARNLLSSHQRMMNSFNPFLVNTYGAFGSICRTRREVVIEGTDES

HP NASAPDAMWEDYEFKCKPGDPSRRPCLISPYHYRLDWLMWFAAFQTYEHNDWI IHLAKL

*... *... *

20

MT -PITEQTVWKAYEFKKGKPGDPRRLPRQWAPYHLRLDWLMWFAAISPGYALPWMTPLNRL ...

HP LASDAEALSLLAHNPFAGRPPPRWVRGEHYRYKFSRPGGRHAAEGKWWVRKRI GAYFPPL

* * * * *

MT LRNDPATLKLLRHNPFP-QSPPRYVRAQLYQYRFTTVAELRRDRA-WWHRTLIGRYVPPM

25

HP SLEELRPYFRDRGWPLPGPL

**

MT SLRKVASPPAD

5

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA019047) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP03877> (SEQ ID NOS: 124, 134 and 144)

Determination of the whole base sequence of the cDNA insert of clone HP03877 obtained from cDNA library of human kidney revealed the structure consisting of a 106-bp 5'-untranslated region, a 1221-bp ORF, and a 678-bp 3'-untranslated region. The ORF encodes a protein consisting of 406 amino acid residues and there existed four putative transmembrane domains. Figure 44 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 49 kDa that was somewhat larger than the molecular weight of 46,208 predicted from the ORF.

The search of the protein database using the amino acid sequence of the present protein revealed that the protein was similar to *Caenorhabditis elegans* hypothetical protein Y37D8A (Accession No. CAA21543). Table 31 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and *Caenorhabditis elegans* hypothetical protein Y37D8A (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 50.2% in the intermediate region of 329 amino acid residues.

15 Table 31.

HP MAENG

CE MAKKQKKSTKSEKERTVEFKPPKPANSEERLVSTRQFLAKIGQKKLIKVKVKNFRFSKKT

20 HP KNCDQRRVAMNKEHHNGNFTDPSSVNEKKRREREERQNIVLWRQPLITLQYFSLEILVIL

* ** . ** . ** . * * . . * . ** .

CE FIDFFSENQKKNCRLKPAGRGMKPPSPSQNTLNRMERETIVFWRRPHIVIPYALMEIAHLA

25 HP KEWTSKLWHRQSIVVSFLLLLAVLIATYYYEGVHQYYVQRIEQFLLYAYWIGLGILSSV

* . * * . * . * . * . . * . * . * .
CE VELFFKILAHKTVLLLT AISIGLAVYGYHAPGAHQEHVQTIKHLWWSWWVLLGVLSSI
HP GLGTGLHTFLLYLGPHIASVTLAAYECNSVNFPEPPYPDQIICPDEEGTEGTISLWSIIS
5 ***. *****. *****. **. *****. * . **. *****. * ** * * .
CE GLGSGLHTFLIYLGPHIAAVTMAAYECQSLDFPQPPYPESIQCPSTKSSI-AVTFWQIVA
HP KVRIEACMWGIGTAIGELPPYFMARAARLSGAEPDDEEYQEFEEML—EHAESAQDFA—
. * . ** ***. **. *****. ** * * . .
10 CE KVRVESLLWGAGTALGELPPYFMARAARISGQEPDDEEYREFLELMNADKESDADQKLSI
HP -SRAKLAVQKLVQKVGFFGILACASIPNPLFDLAGITCGHFLVPFWTFFGATLIGKAIK
*** * ** *** *****. *****. *
CE VERAKSWVEHNIHRLGFP GILLFASIPNPLFDLAGITCGHFLVPFWSFFGATLIGKALVK
15 HP MHIQKIFVIITFSKHIVEQMVAFIGAVPGIGPSLQKPFQYLEAQRQKLHHKSEMGTPOG
** . * . ***. ** . * . * . . . * . ** . . * . . ** ** . ** . . . * .
CE MHVQMGFVILAFSDHHAENFVKILEKIPAVGPYIRQPISDLLEKQRKALHKTPGEHSEQD
20 HP ENWLSWMFEKLVVVMVCYFILSIINSMASQYAKRIQQRNLNSEEKTK
CE LIDEENQSFEFFFFFFAVTPPSSCPLLLS DGFEGVVVKK

of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T18977) among ESTs. However, since they are partial sequences, it can not be judged whether or not they
5 encode the same protein as the protein of the present invention.

<HP10765> (SEQ ID NOS: 125, 135 and 145)

Determination of the whole base sequence of the cDNA insert of clone HP10765 obtained from cDNA library of
10 human umbilical cord blood revealed the structure consisting of a 30-bp 5'-untranslated region, a 1362-bp ORF, and a 166-bp 3'-untranslated region. The ORF encodes a protein consisting of 453 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative
15 transmembrane domain in the inner portion. Figure 45 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 48 kDa that was almost identical with the molecular
20 weight of 47,724 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. A1792834) among ESTs. However, since they are
25 partial sequences, it can not be judged whether or not they

encode the same protein as the protein of the present invention.

<HP10766> (SEQ ID NOS: 126, 136 and 146)

Determination of the whole base sequence of the
5 cDNA insert of clone HP10766 obtained from cDNA library of
human kidney revealed the structure consisting of a 150-bp
5'-untranslated region, a 180-bp ORF, and a 675-bp 3'-
untranslated region. The ORF encodes a protein consisting of
59 amino acid residues and there existed two putative
10 transmembrane domains. Figure 46 depicts the
hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of 10 kDa or less that was almost identical with the
15 molecular weight of 6,098 predicted from the ORF.

The search of the GenBank using the base sequences
of the present cDNA has revealed the registration of
sequences that shared a homology of 90% or more (for example,
Accession No. T85491) among ESTs. However, since they are
20 partial sequences, it can not be judged whether or not they
encode the same protein as the protein of the present
invention.

<HP10770> (SEQ ID NOS: 127, 137 and 147)

Determination of the whole base sequence of the
25 cDNA insert of clone HP10770 obtained from cDNA library of

human kidney revealed the structure consisting of a 150-bp 5'-untranslated region, a 633-bp ORF, and a 186-bp 3'-untranslated region. The ORF encodes a protein consisting of 210 amino acid residues and there existed two putative transmembrane domains. Figure 47 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was larger than the molecular weight of 22,156 predicted from the ORF.

The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI792771) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10772> (SEQ ID NOS: 128, 138 and 148)

Determination of the whole base sequence of the cDNA insert of clone HP10772 obtained from cDNA library of human kidney revealed the structure consisting of a 19-bp 5'-untranslated region, a 498-bp ORF, and a 724-bp 3'-untranslated region. The ORF encodes a protein consisting of 165 amino acid residues and there existed four putative transmembrane domains. Figure 48 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

5 The search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. F11871) among ESTs. However, since they are partial sequences, it can not be judged whether or not they
10 encode the same protein as the protein of the present invention.

 <HP10773> (SEQ ID NOS: 129, 139 and 149)

 Determination of the whole base sequence of the cDNA insert of clone HP10773 obtained from cDNA library of
15 human kidney revealed the structure consisting of a 186-bp 5'-untranslated region, a 489-bp ORF, and a 499-bp 3'-untranslated region. The ORF encodes a protein consisting of 162 amino acid residues and there existed four putative transmembrane domains. Figure 49 depicts the
20 hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

 The search of the GenBank using the base sequences
25 of the present cDNA has revealed the registration of

sequences that shared a homology of 90% or more (for example, Accession No. N33828) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

<HP10776> (SEQ ID NOS: 130, 140 and 150) :

Determination of the whole base sequence of the cDNA insert of clone HP10776 obtained from cDNA library of human kidney revealed the structure consisting of a 207-bp 5'-untranslated region, a 666-bp ORF, and a 139-bp 3'-untranslated region. The ORF encodes a protein consisting of 221 amino acid residues and there existed three putative transmembrane domains. Figure 50 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was larger than the molecular weight of 24,883 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AI929639) among ESTs. However, since they are partial sequences, it can not be judged whether or not they encode the same protein as the protein of the present invention.

INDUSTRIAL APPLICABILITY

The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs and eukaryotic cells expressing these DNAs. Since all of the proteins of the present invention are secreted or exist in the cell membrane, they are considered to be proteins controlling the proliferation and/or the differentiation of the cells. Accordingly, the proteins of the present invention can be employed as pharmaceuticals such as carcinostatic agents which act to control the proliferation and/or the differentiation of the cells, or as antigens for preparing antibodies against these proteins. The DNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the DNAs can be utilized for expressing these proteins in large quantities. Cells into which these genes are introduced to express these proteins can be utilized for detection of the corresponding receptors or ligands, screening of novel small molecule pharmaceuticals and the like. The antibody of the present invention can be utilized for the detection, quantification, purification and the like of the protein of the present invention.

The present invention also provides genes

corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include
5 contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements.

10 The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate
15 genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified
20 expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene. (Albert and
25 Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254;

Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, Bioessays 14(9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA 90(16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci. USA 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination,

preferably detected by positive/negative genetic selection strategies (Mansour et al., 1988, Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are
5 incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development
10 of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s). Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such
15 forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known
20 techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and
25 most preferably at least 75%) of the length of a disclosed

protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide, as determined by those of skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is,

naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the polynucleotides.

5 The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

 The present invention also includes polynucleotides capable of hybridizing under reduced
10 stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for
15 example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 32

Stringency Condition	Poly-nucleotide Hybrid	Hybrid Length (bp) ¹	Hybridization Temperature and Buffer ¹	Wash Temperature and Buffer ¹
A	DNA : DNA	≥50	65°C; 1×SSC -or- 42°C; 1×SSC, 50% formamide	65°C; 0.3×SSC
B	DNA : DNA	<50	T _B *; 1×SSC	T _B *; 1×SSC
C	DNA : RNA	≥50	67°C; 1×SSC -or- 45°C; 1×SSC, 50% formamide	67°C; 0.3×SSC
D	DNA : RNA	<50	T _D *; 1×SSC	T _D *; 1×SSC
E	RNA : RNA	≥50	70°C; 1×SSC -or- 50°C; 1×SSC, 50% formamide	70°C; 0.3×SSC
F	RNA : RNA	<50	T _F *; 1×SSC	T _F *; 1×SSC
G	DNA : DNA	≥50	65°C; 4×SSC -or- 42°C; 4×SSC, 50% formamide	65°C; 1×SSC
H	DNA : DNA	<50	T _H *; 4×SSC	T _H *; 4×SSC
I	DNA : RNA	≥50	67°C; 4×SSC -or- 45°C; 4×SSC, 50% formamide	67°C; 1×SSC
J	DNA : RNA	<50	T _J *; 4×SSC	T _J *; 4×SSC
K	RNA : RNA	≥50	70°C; 4×SSC -or- 50°C; 4×SSC, 50% formamide	67°C; 1×SSC
L	RNA : RNA	<50	T _L *; 2×SSC	T _L *; 2×SSC
M	DNA : DNA	≥50	50°C; 4×SSC -or- 40°C; 6×SSC, 50% formamide	50°C; 2×SSC
N	DNA : DNA	<50	T _N *; 6×SSC	T _N *; 6×SSC
O	DNA : RNA	≥50	55°C; 4×SSC -or- 42°C; 6×SSC, 50% formamide	55°C; 2×SSC
P	DNA : RNA	<50	T _P *; 6×SSC	T _P *; 6×SSC
Q	RNA : RNA	≥50	60°C; 4×SSC -or- 45°C; 6×SSC, 50% formamide	60°C; 2×SSC
R	RNA : RNA	<50	T _R *; 4×SSC	T _R *; 4×SSC

* : The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

10 † : SSPE (1×SSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

15 *T_B - T_R : The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length,
20 T_m(°C)=2(#of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C)=81.5 + 16.6(log₁₀[Na⁺]) + 0.41 (%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for
25 1×SSC=0.165M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

10 Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more
15 preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and
20 identity while minimizing sequence gaps.

CLAIMS

1. A protein comprising any one of an amino acid sequence selected from the group consisting of SEQ ID NOS: 1 to 10, 31 to 40, 61 to 70, 91 to 100 and 121 to 130.

2. An isolated DNA encoding the protein according to Claim 1.

3. An isolated cDNA comprising any one of a base sequence selected from the group consisting of SEQ ID NOS: 11 to 20, 41 to 50, 71 to 80, 101 to 110 and 131 to 140.

4. The cDNA according to Claim 3 consisting of any one of a base sequence selected from the group consisting of SEQ ID NOS: 21 to 30, 51 to 60, 81 to 90, 111 to 120 and 141 to 150.

5. An expression vector that is capable of expressing the DNA according to any one of Claim 2 to Claim 4 by in vitro translation or in eukaryotic cells.

6. A transformed eukaryotic cell that is capable of expressing the DNA according to any one of Claim 2 to Claim 4 and of producing the protein according to Claim 1.

7. An antibody directed to the protein according to Claim 1.

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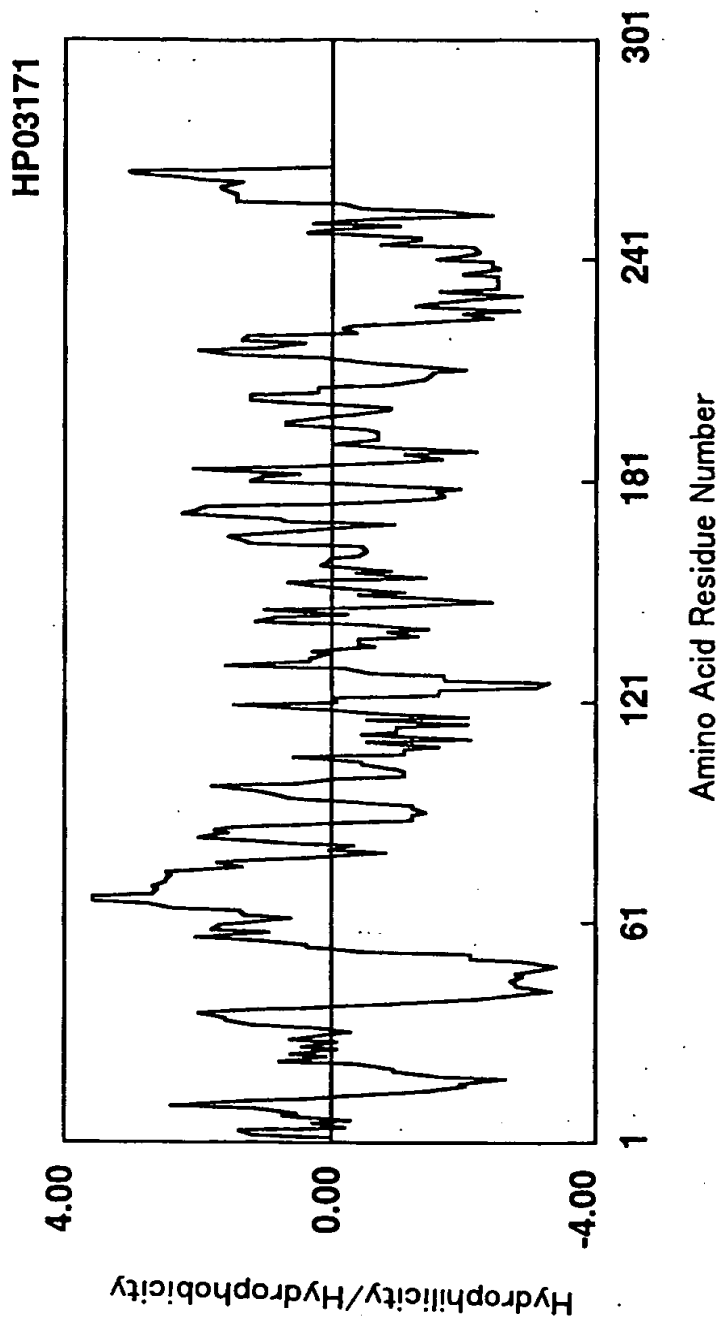


Fig.1

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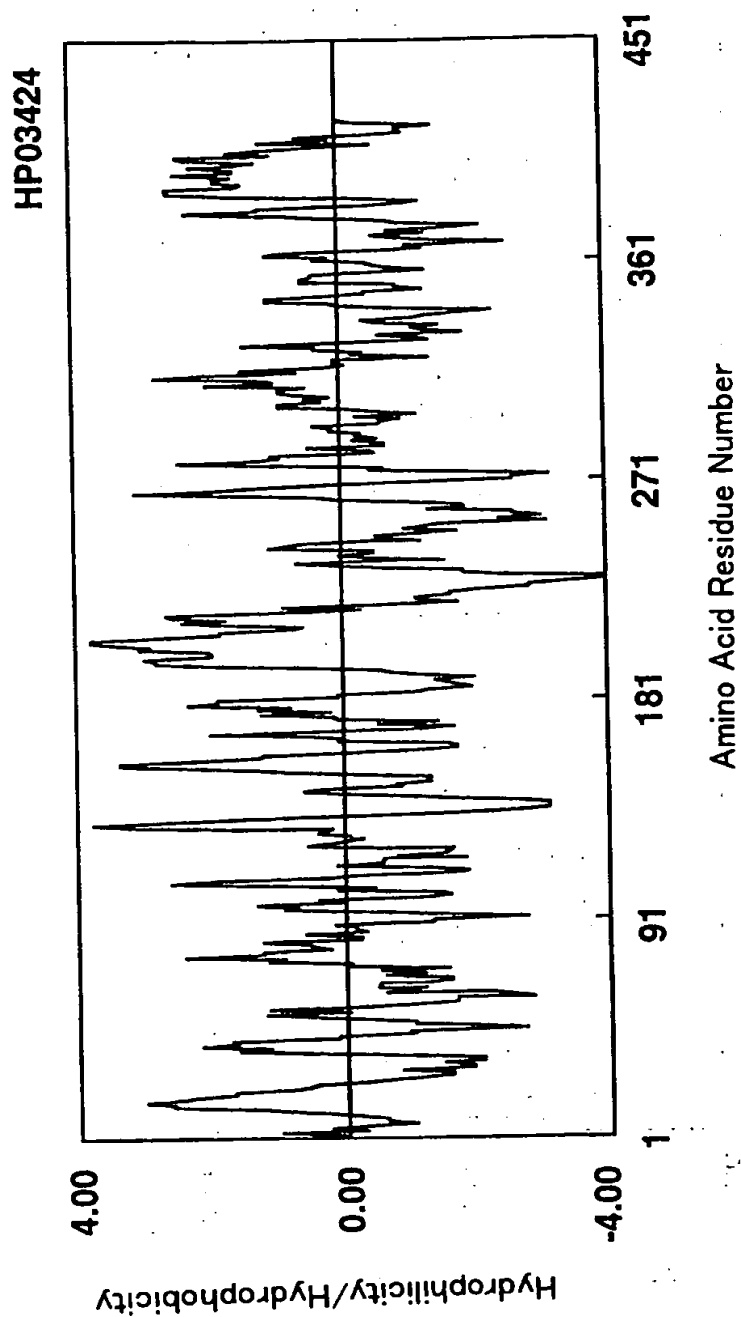


Fig.2

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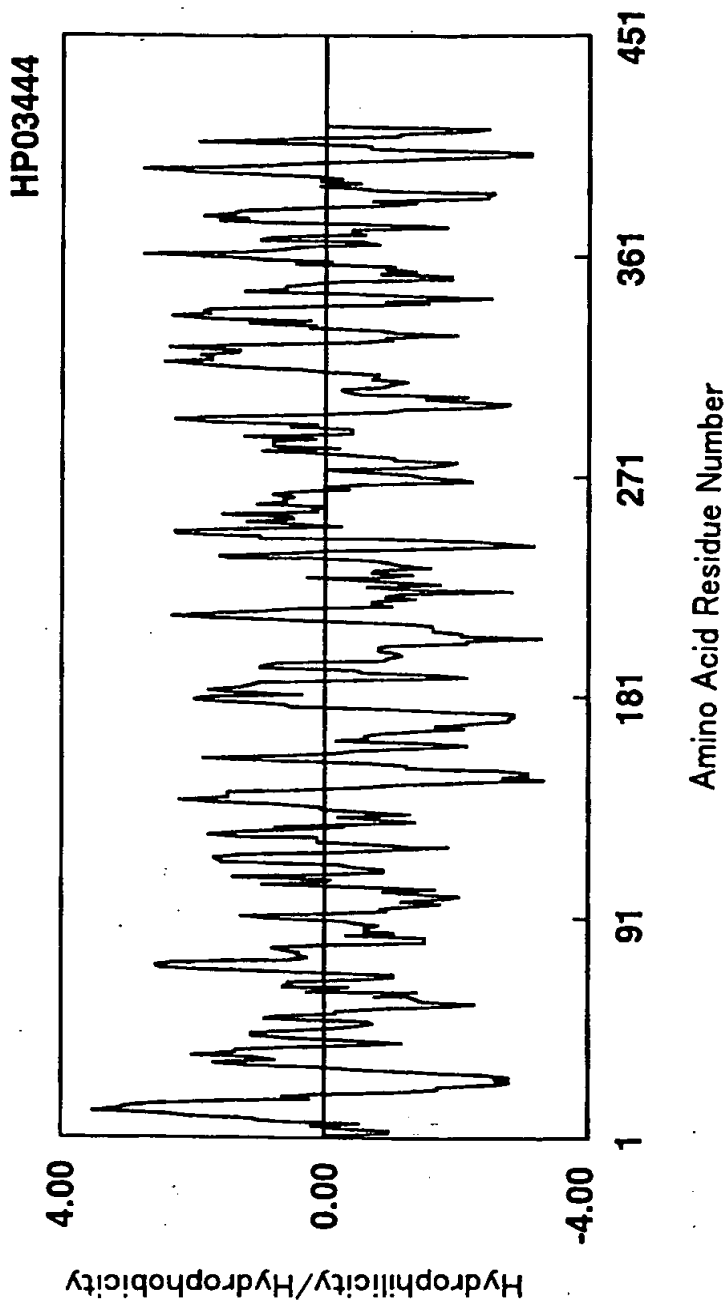


Fig.3

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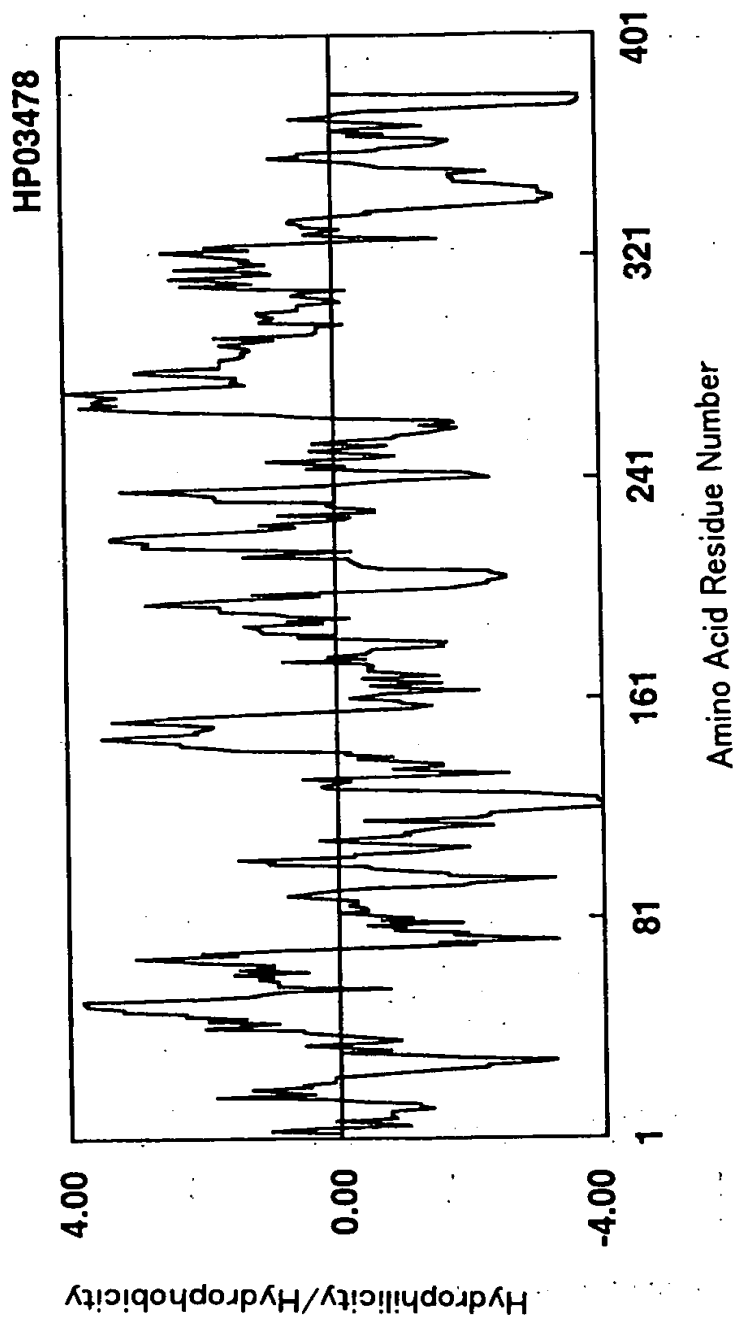


Fig.4

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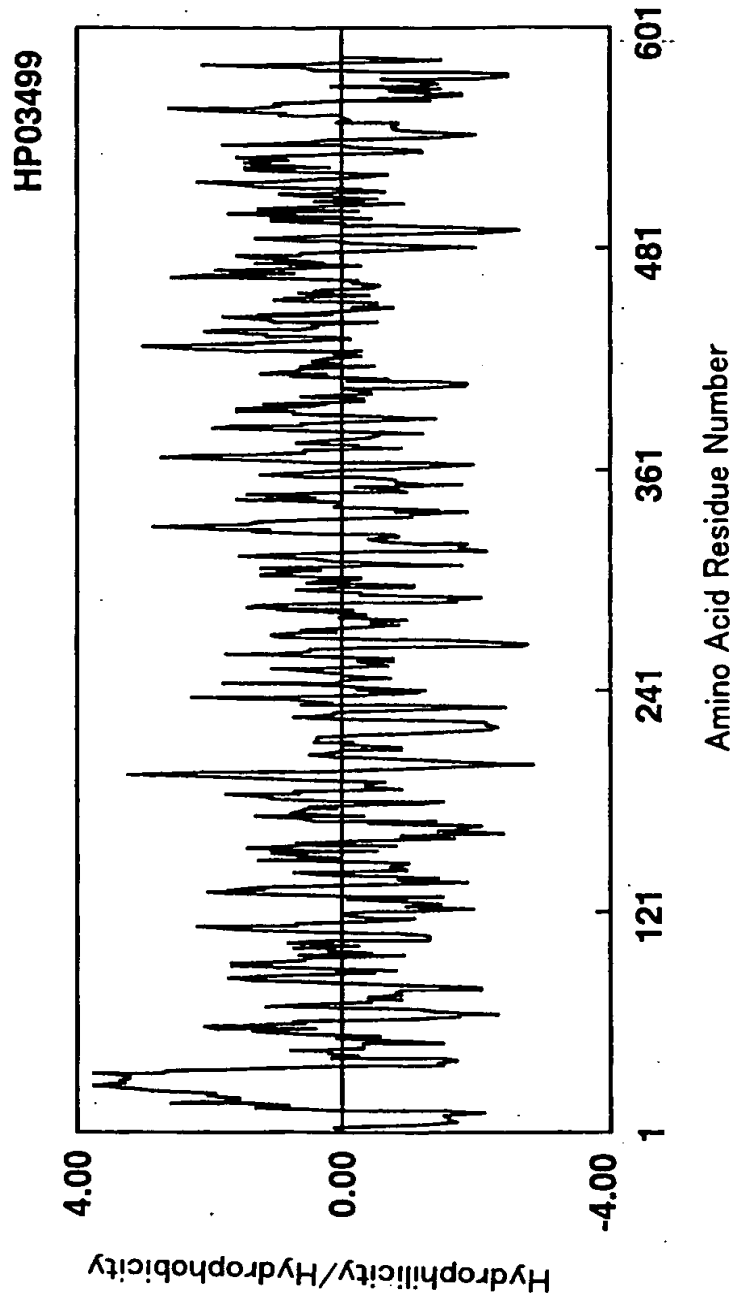


Fig.5

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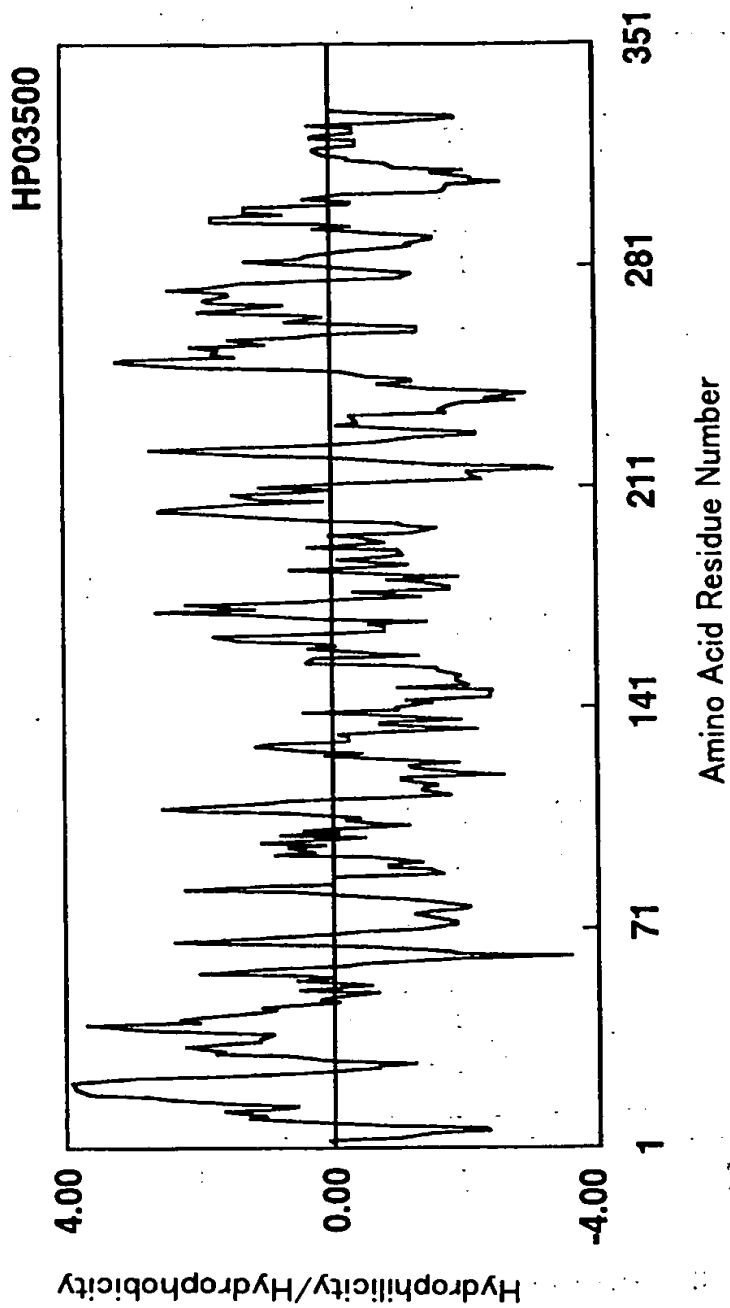


Fig.6

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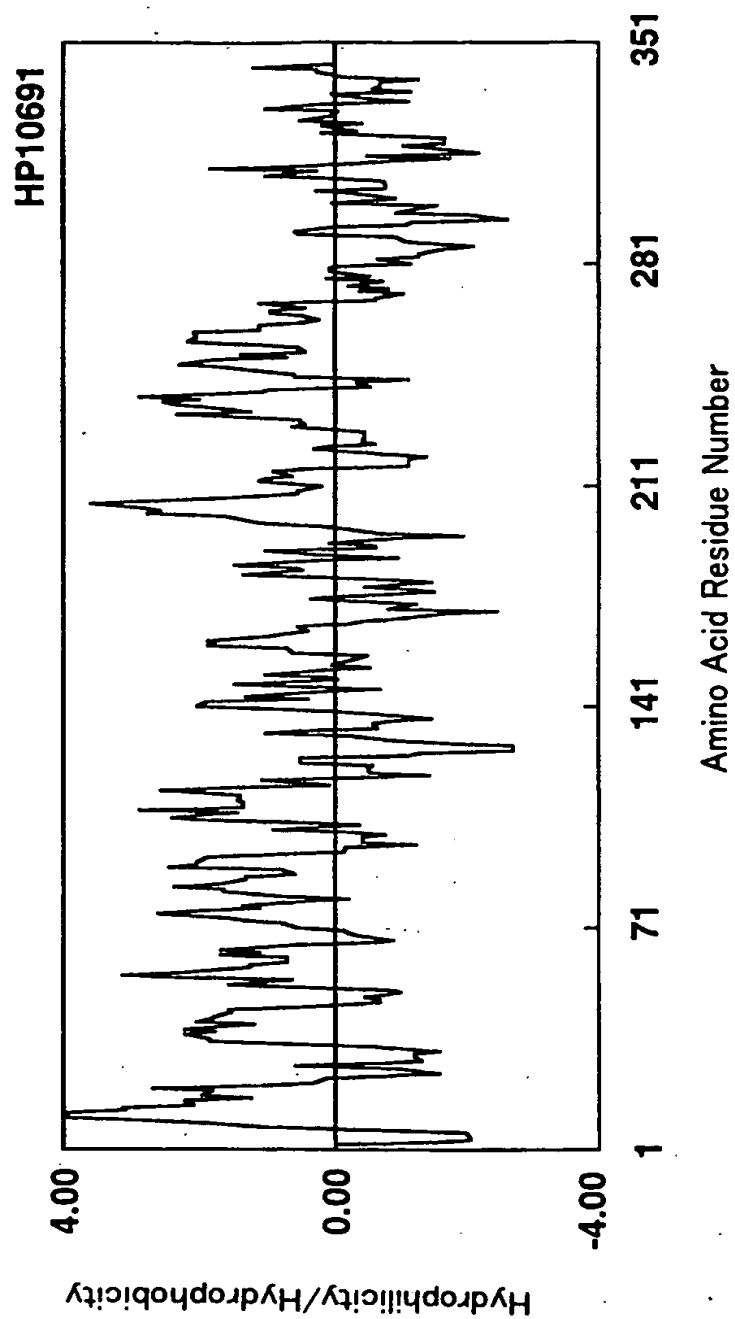


Fig.7

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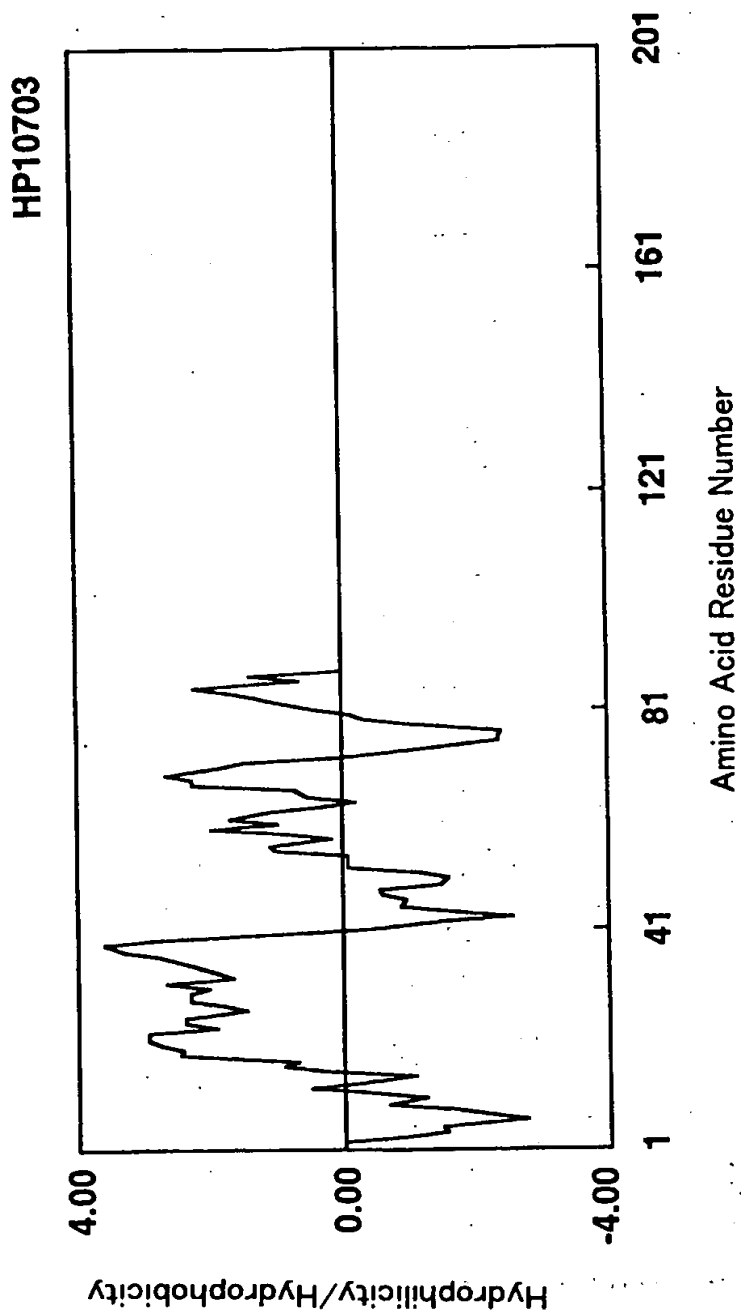


Fig.8

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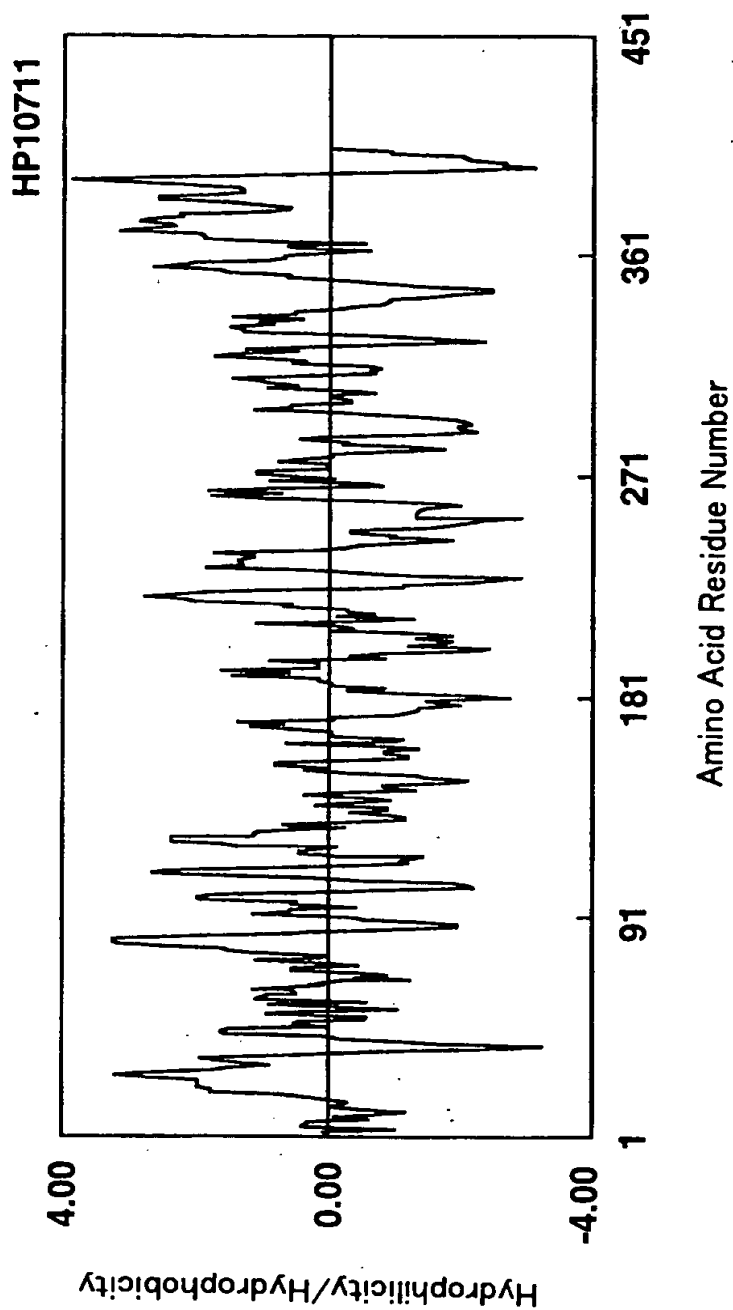


Fig.9

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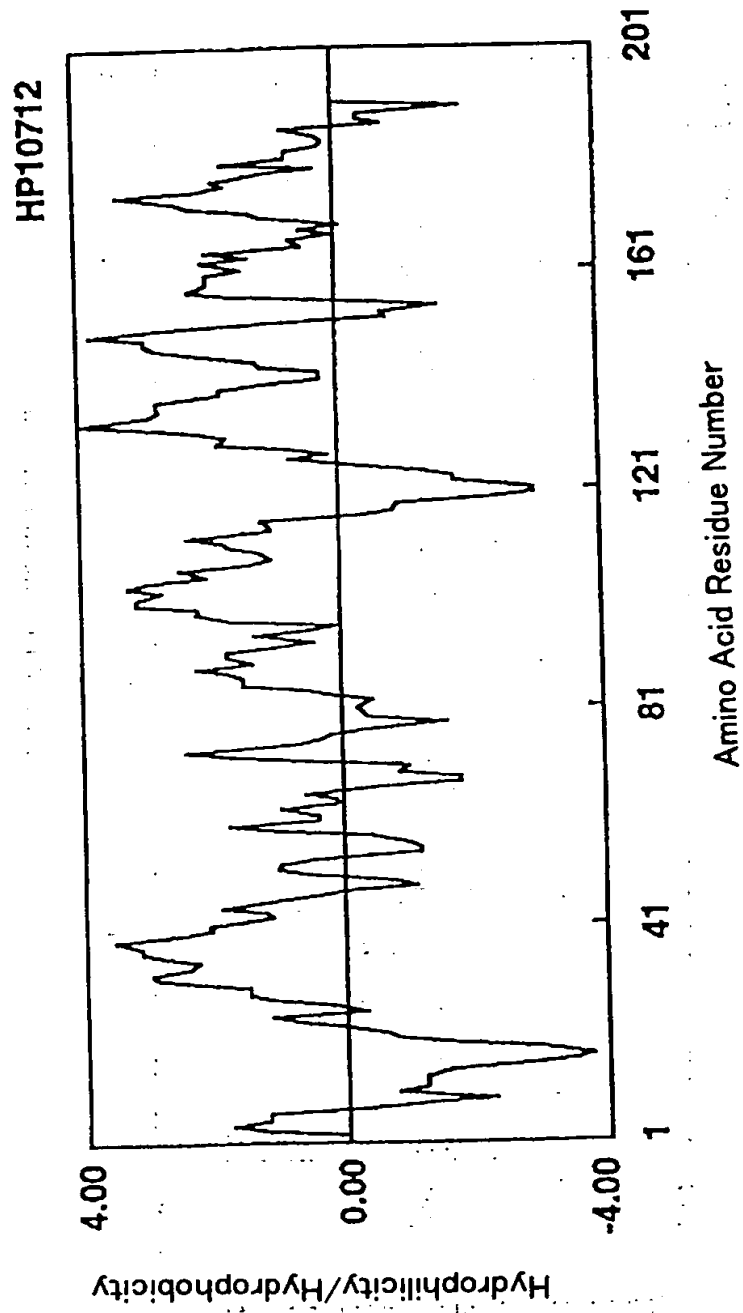


Fig.10

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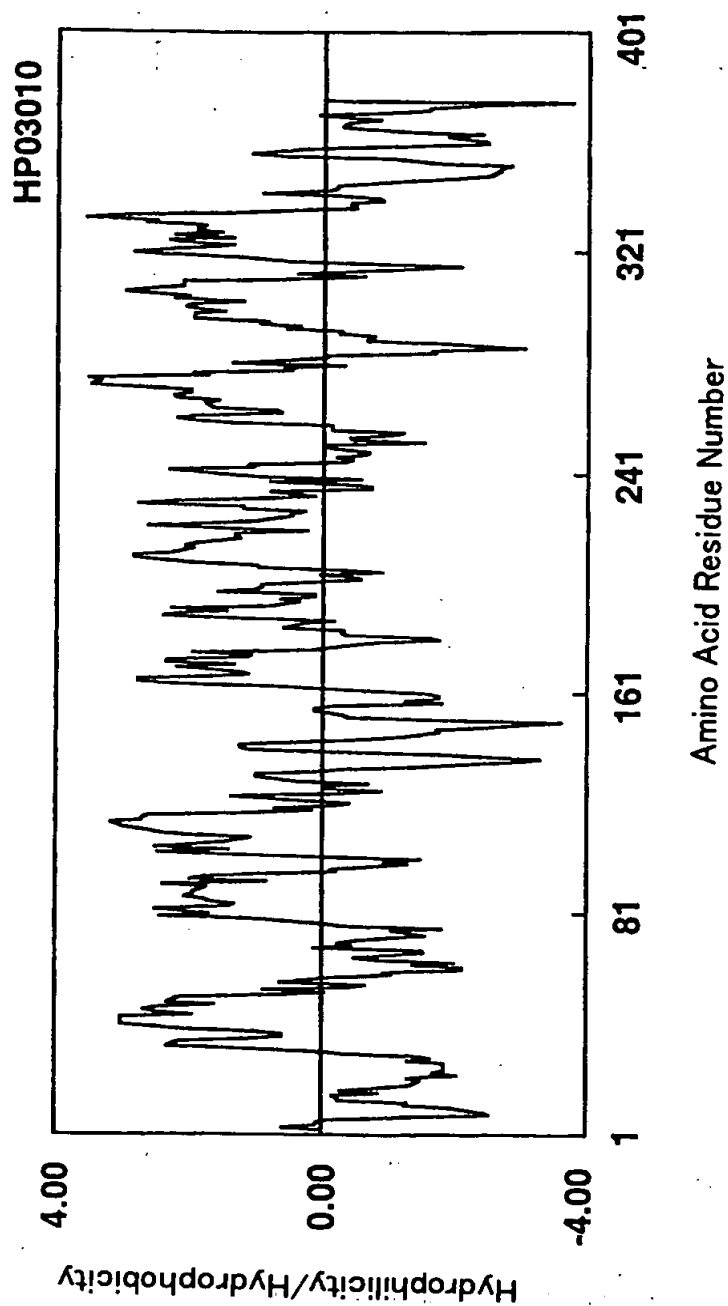


Fig.11

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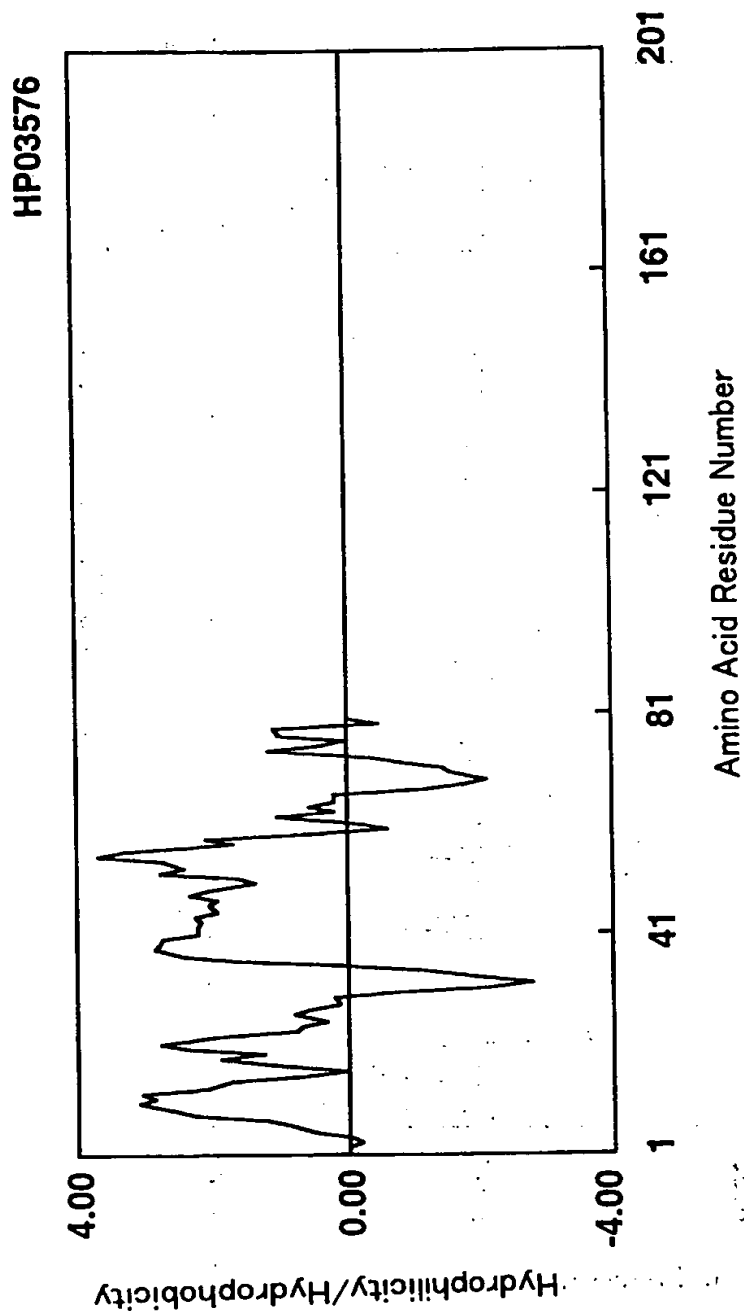


Fig.12

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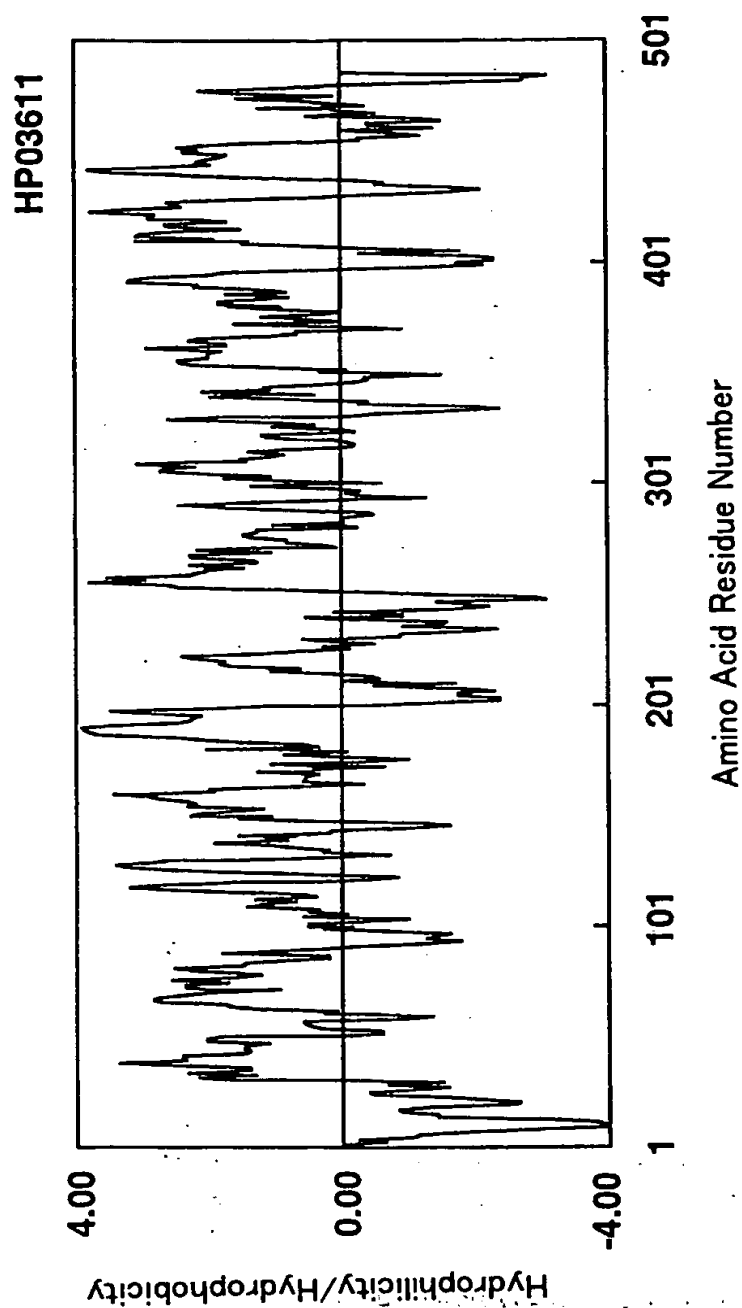


Fig.13

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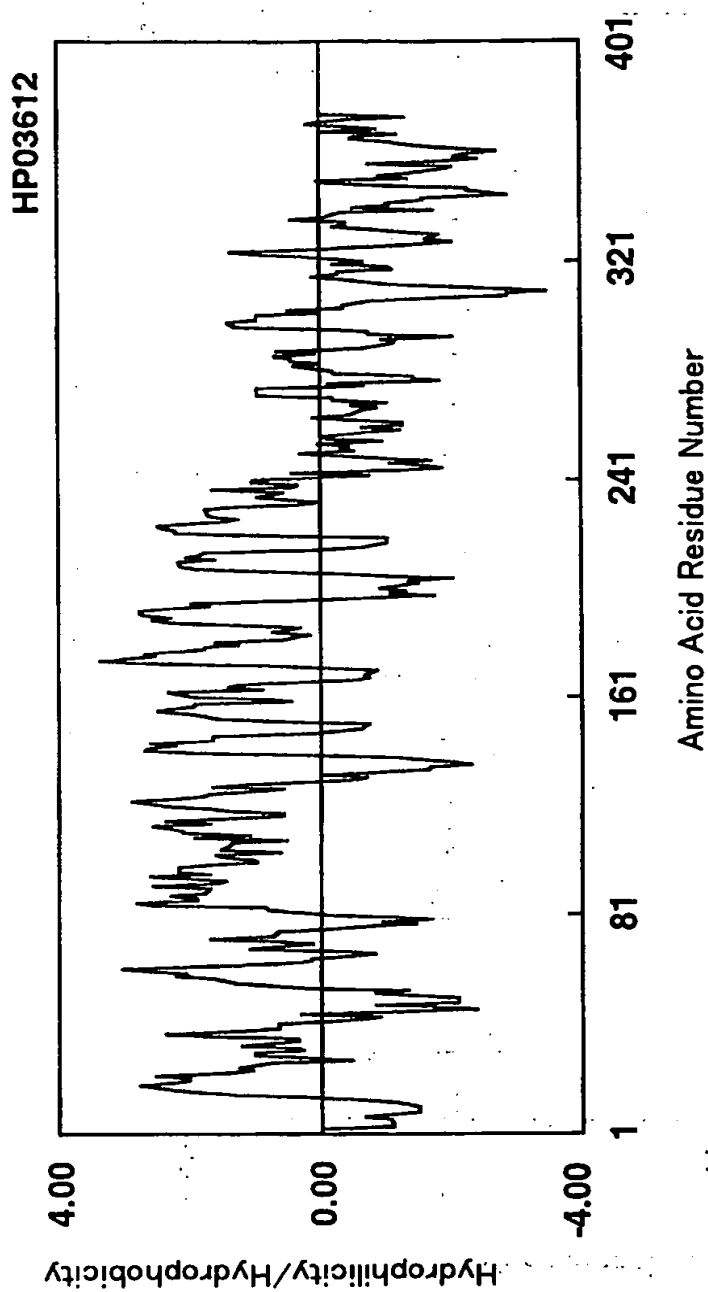


Fig.14

15/50

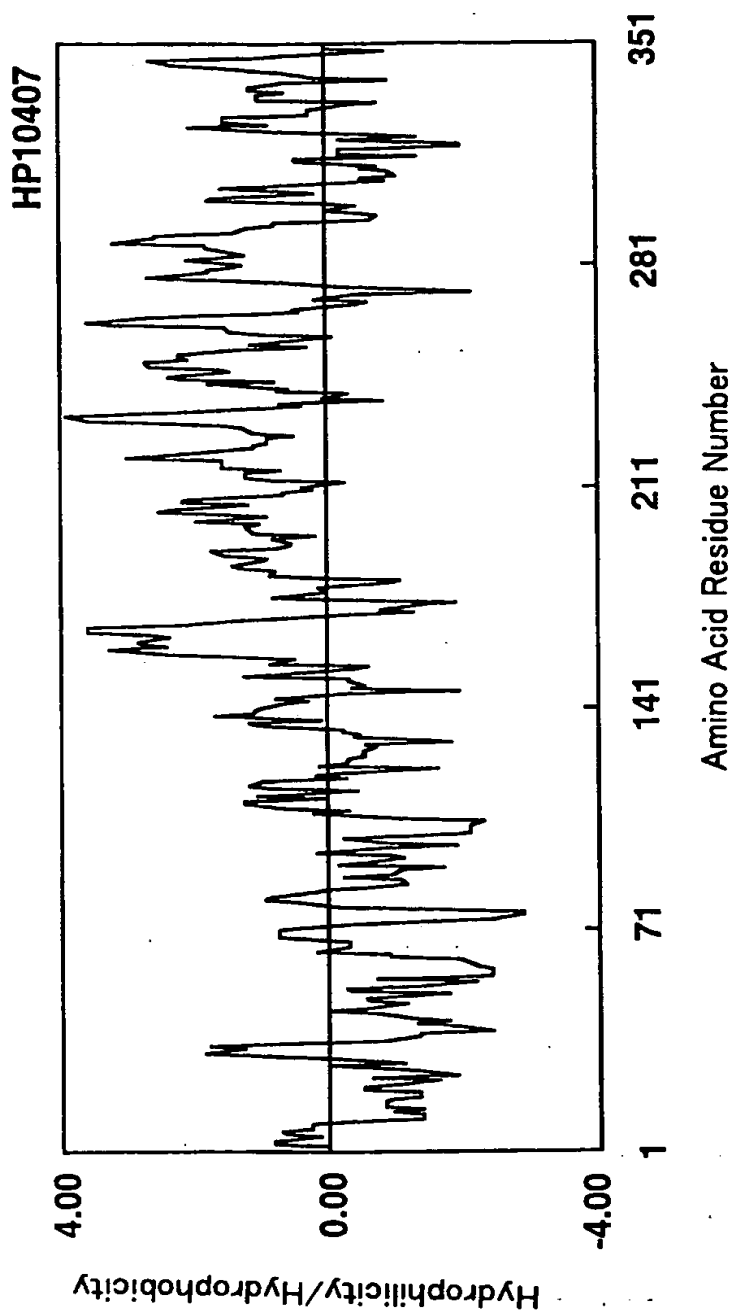


Fig.15

16/50

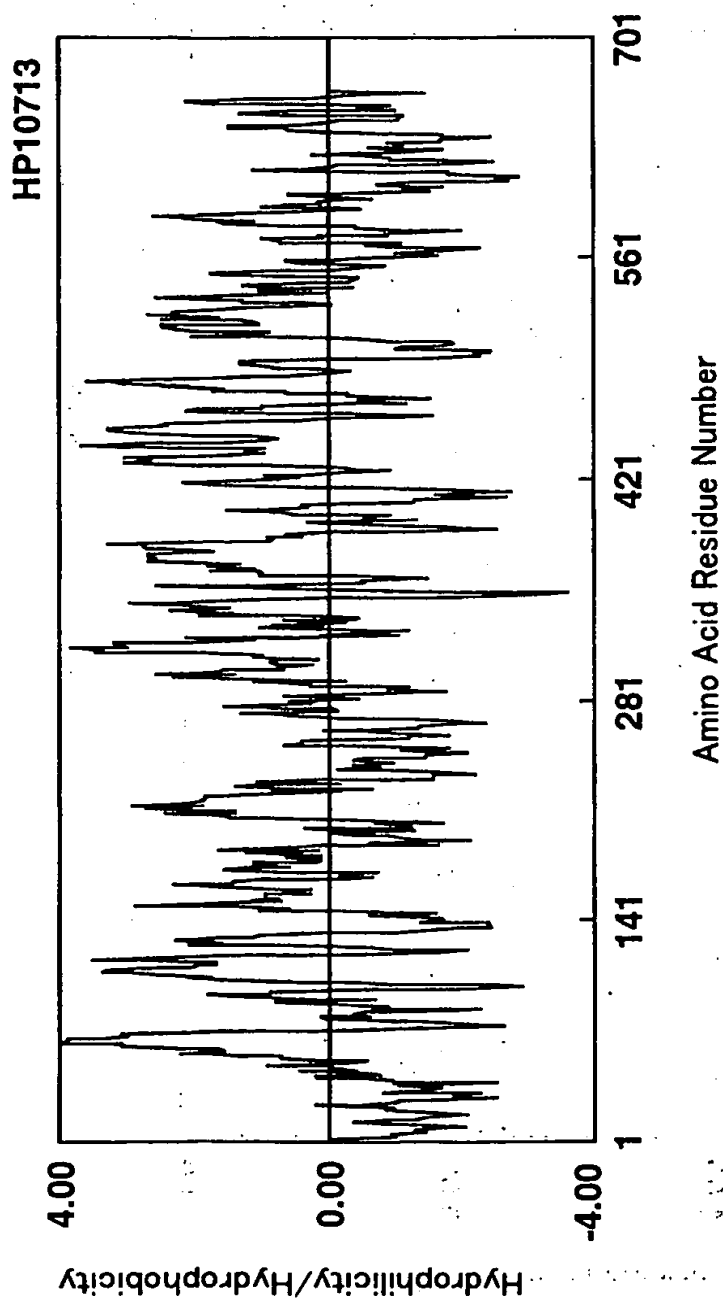


Fig.16

17/50

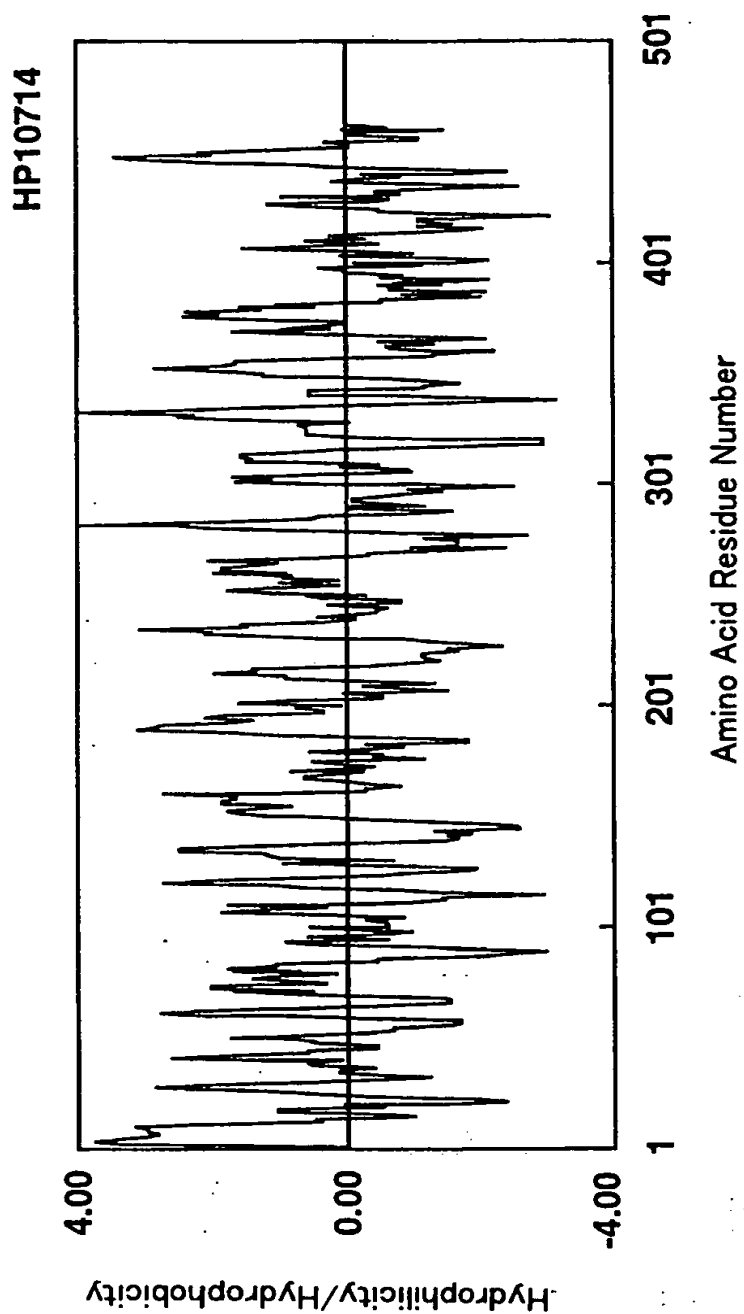


Fig.17

18/50

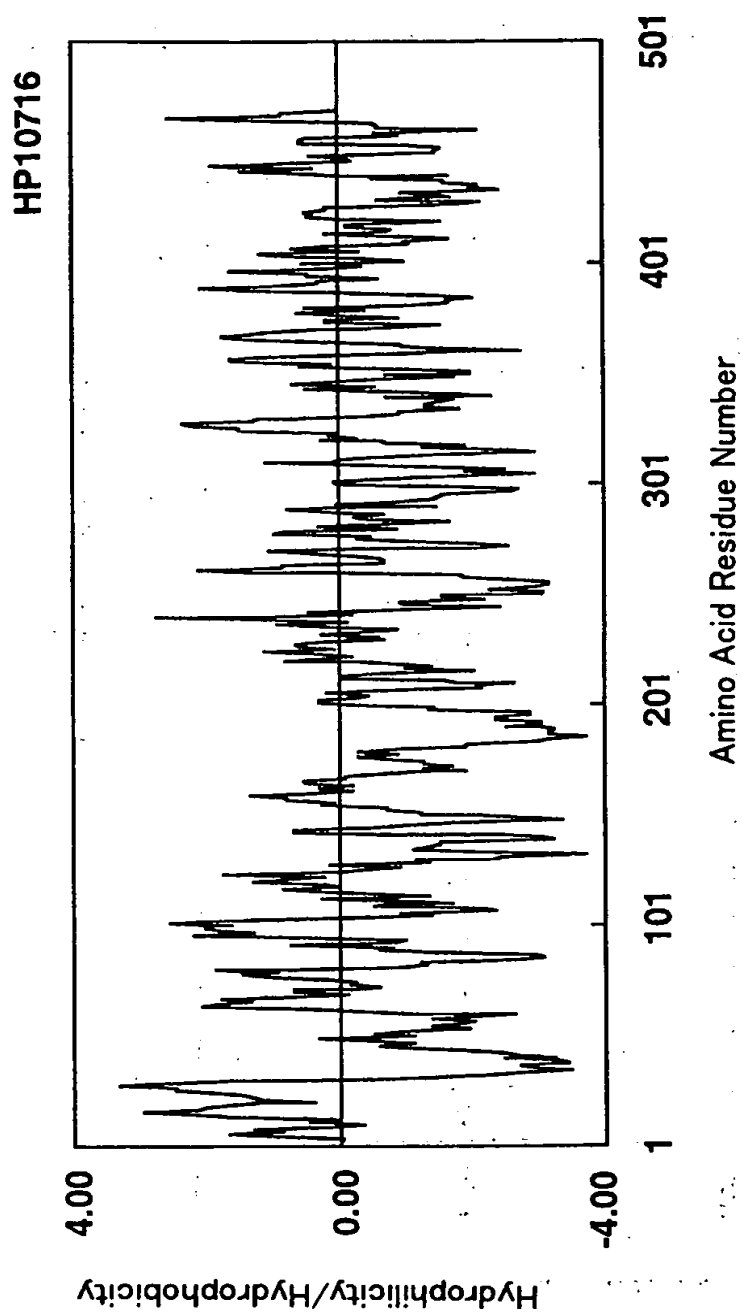


Fig.18

19/50

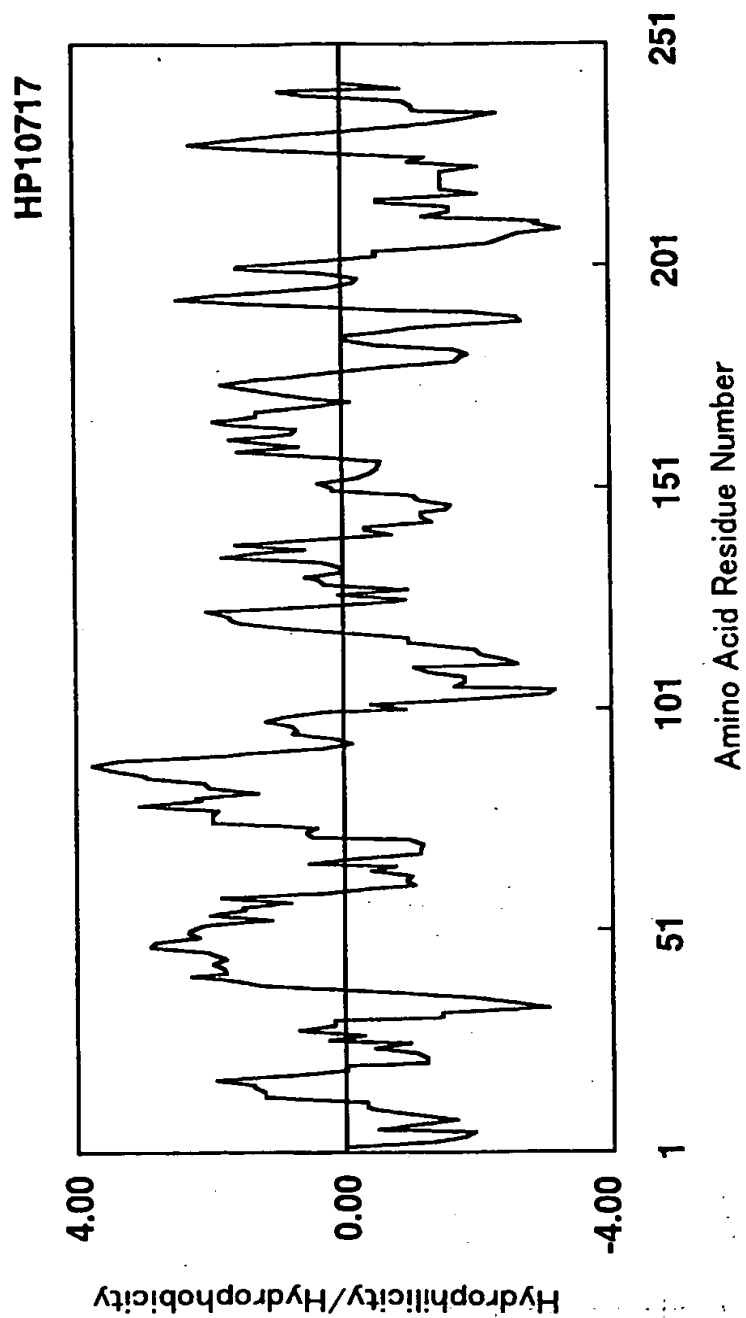


Fig.19

20/50

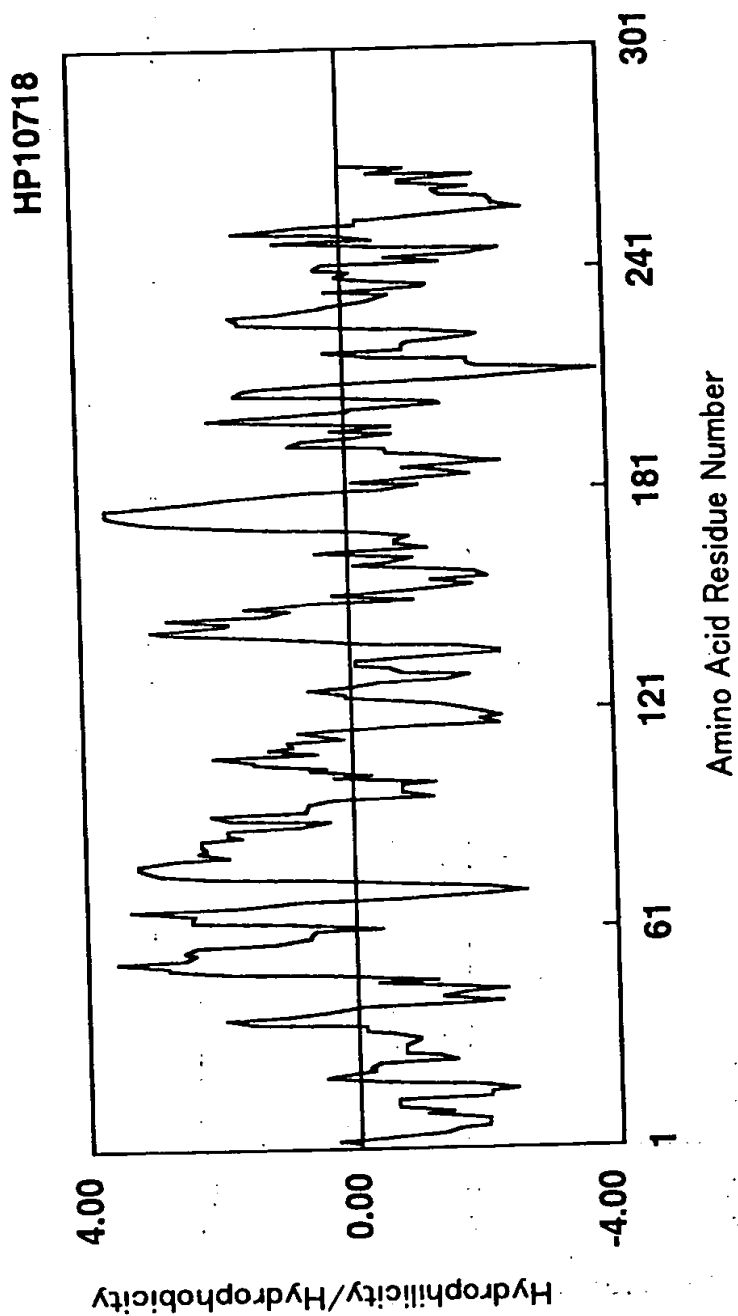


Fig.20

21/50

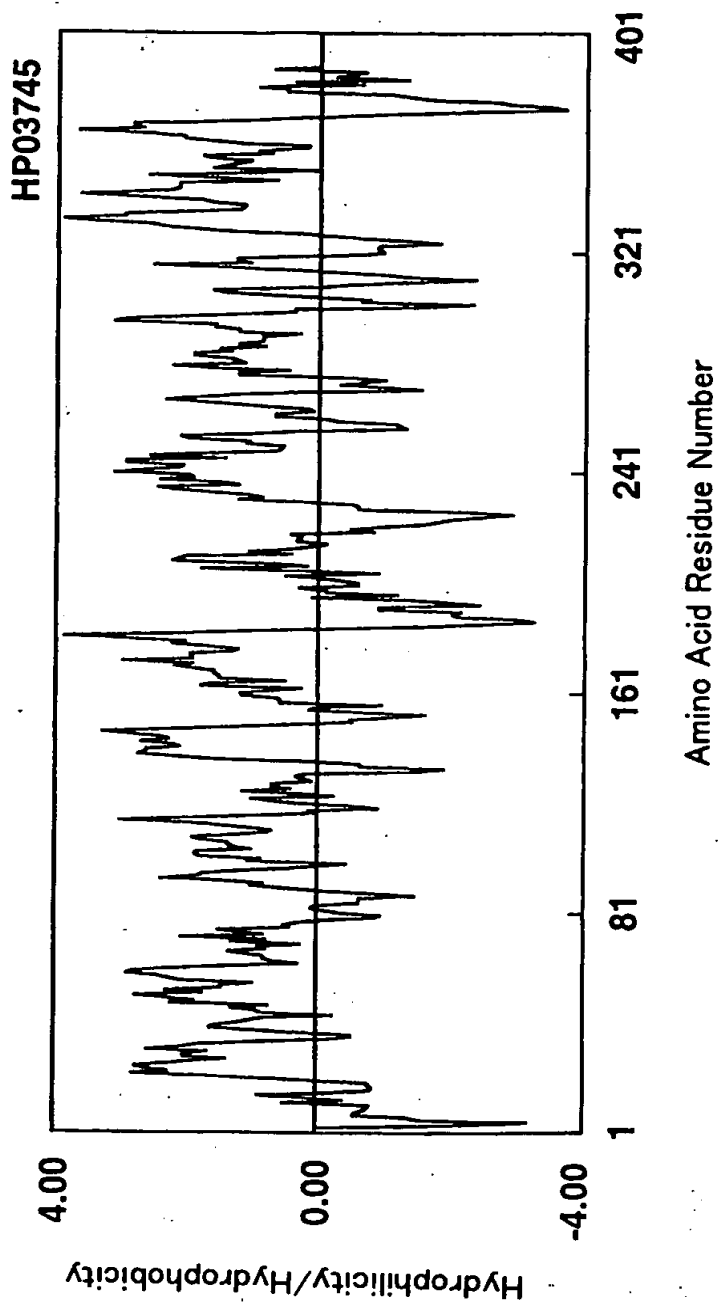


Fig.21

22/50

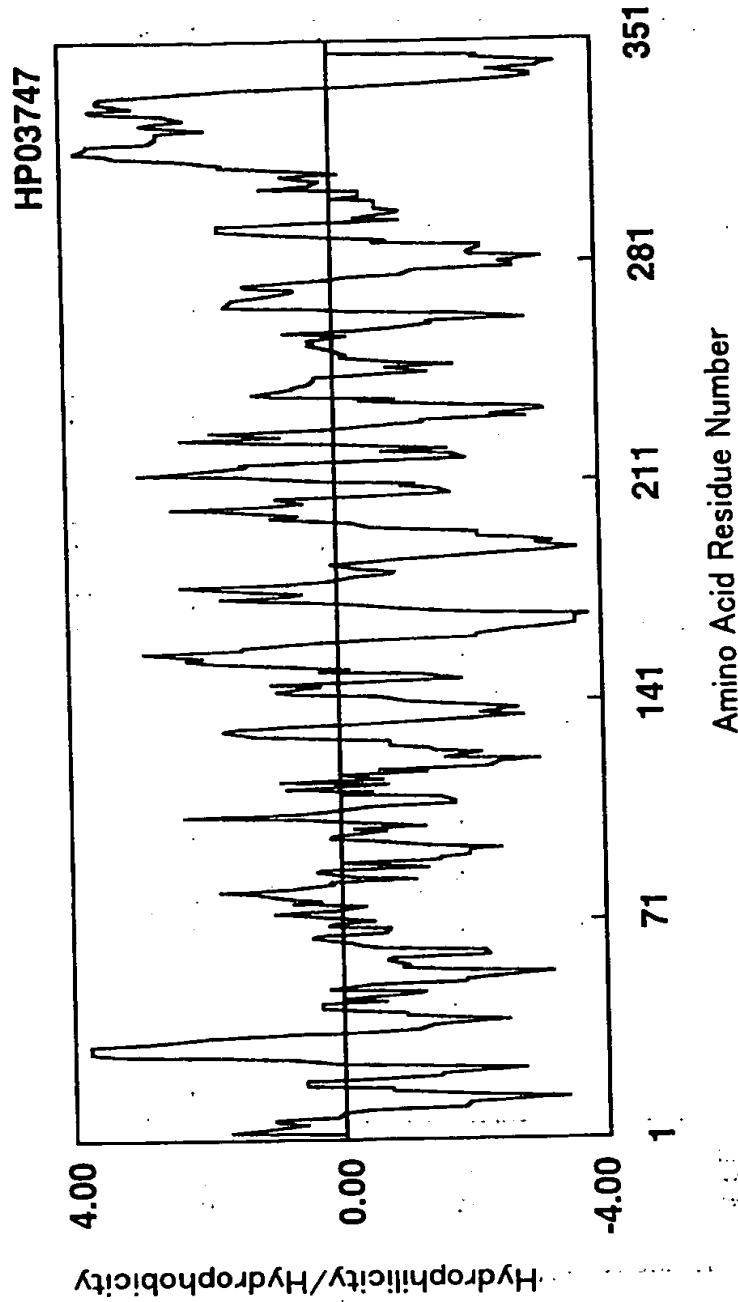


Fig.22

23/50

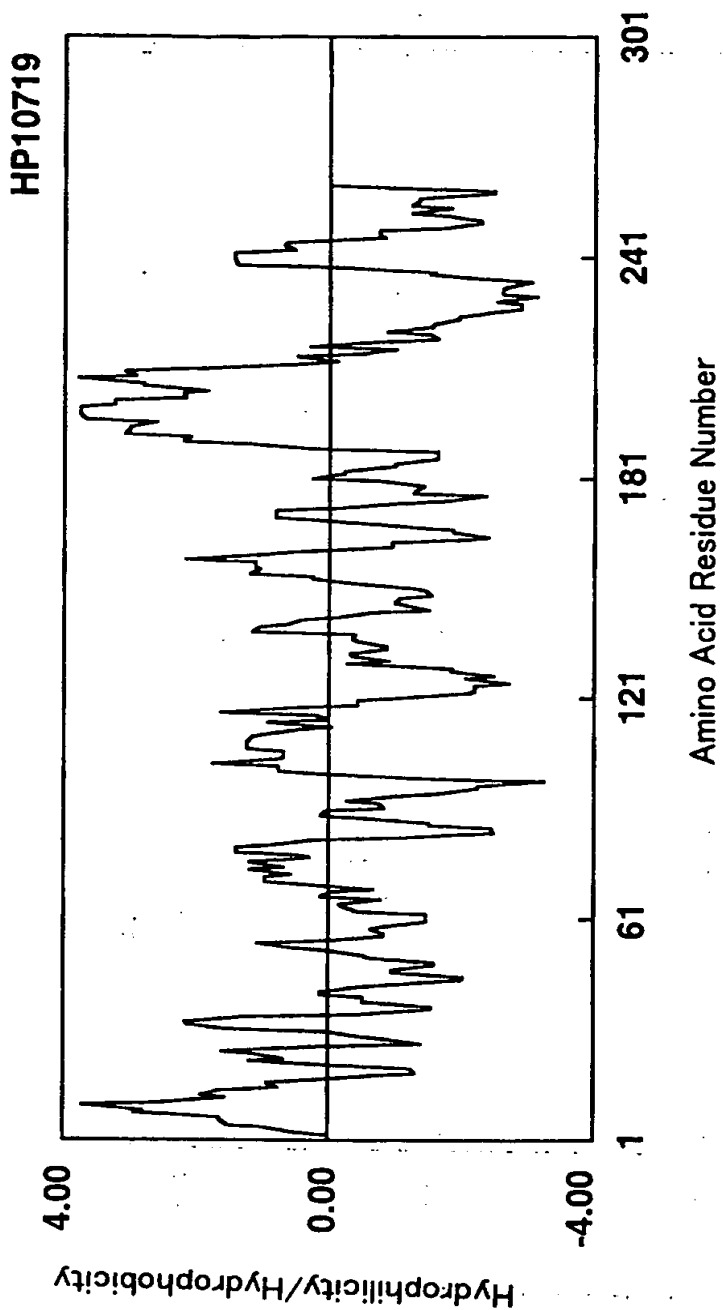


Fig.23

24/50

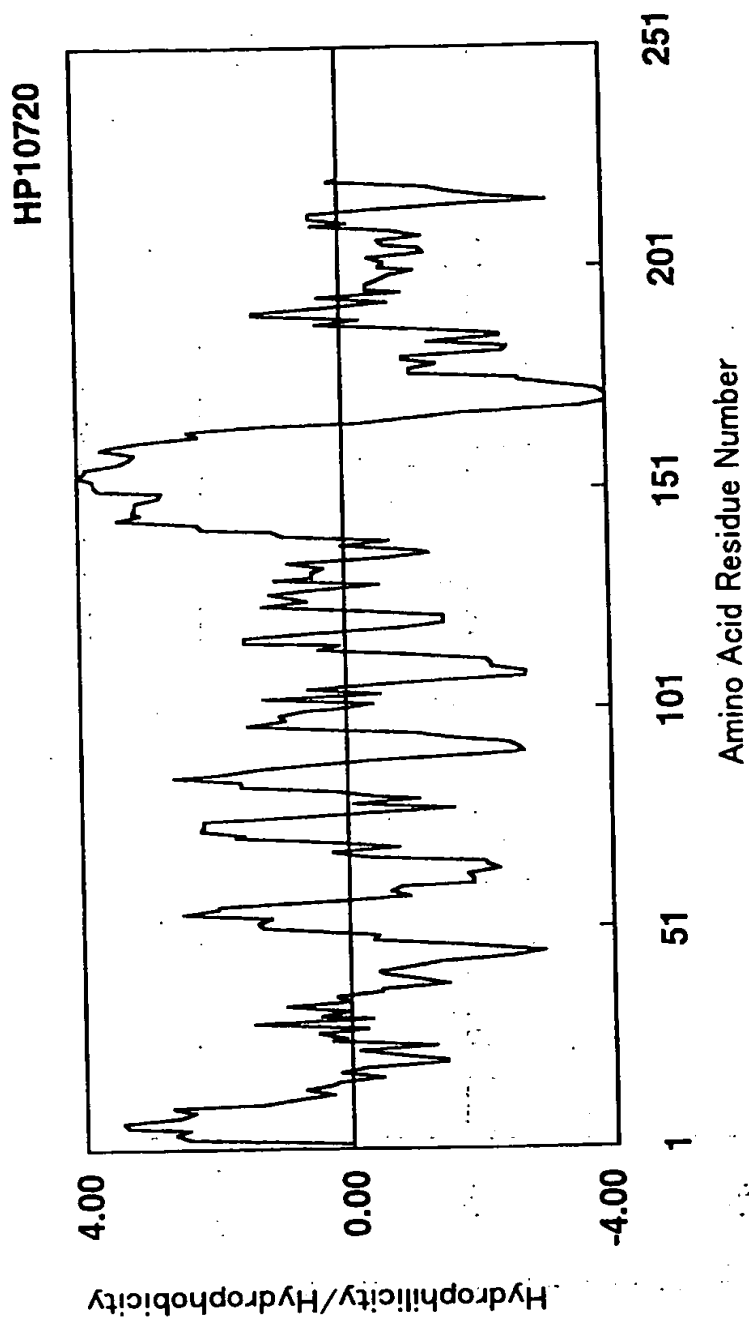


Fig.24

25/50

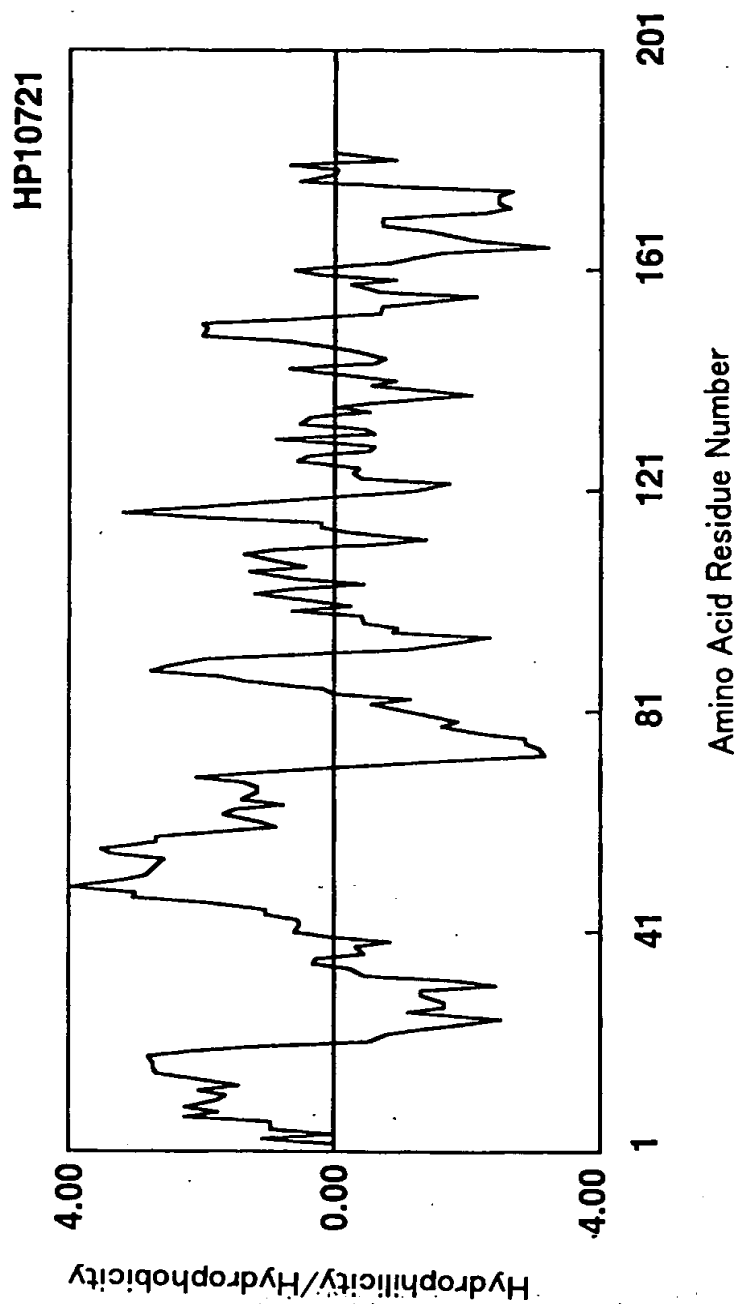


Fig.25

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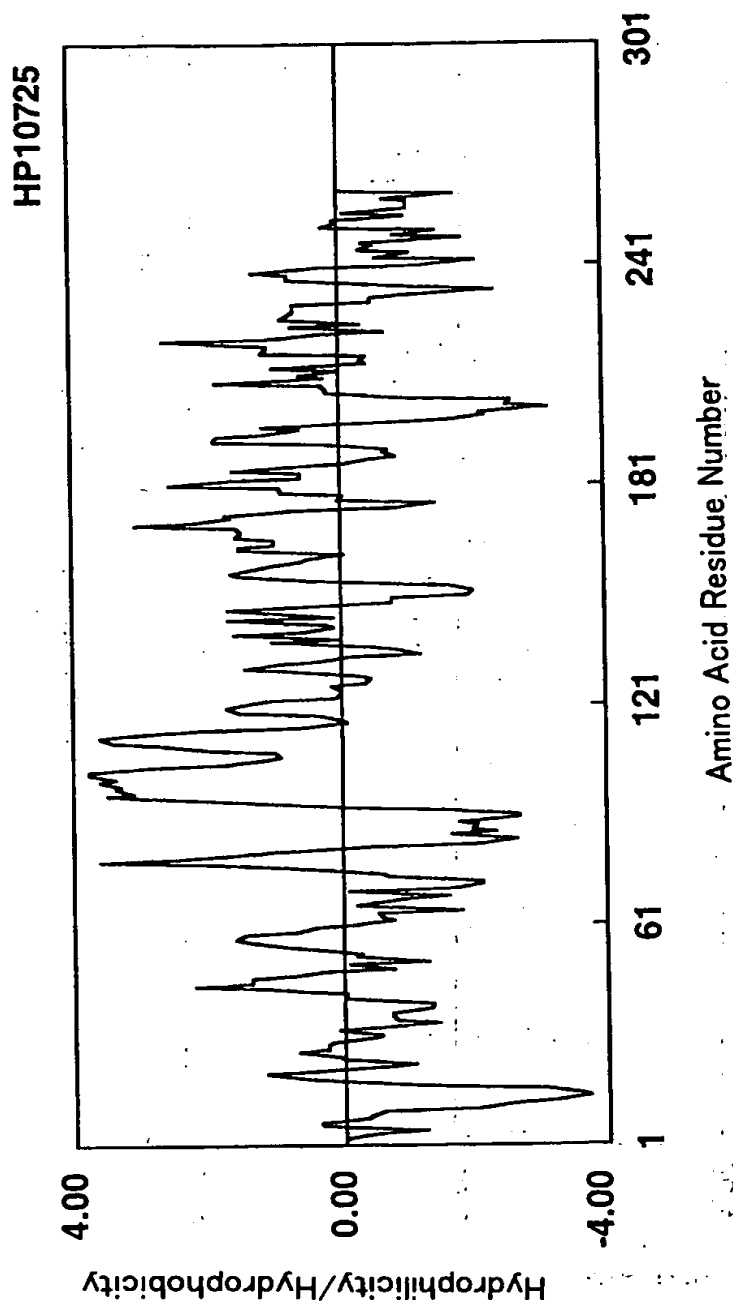


Fig.26

27/50

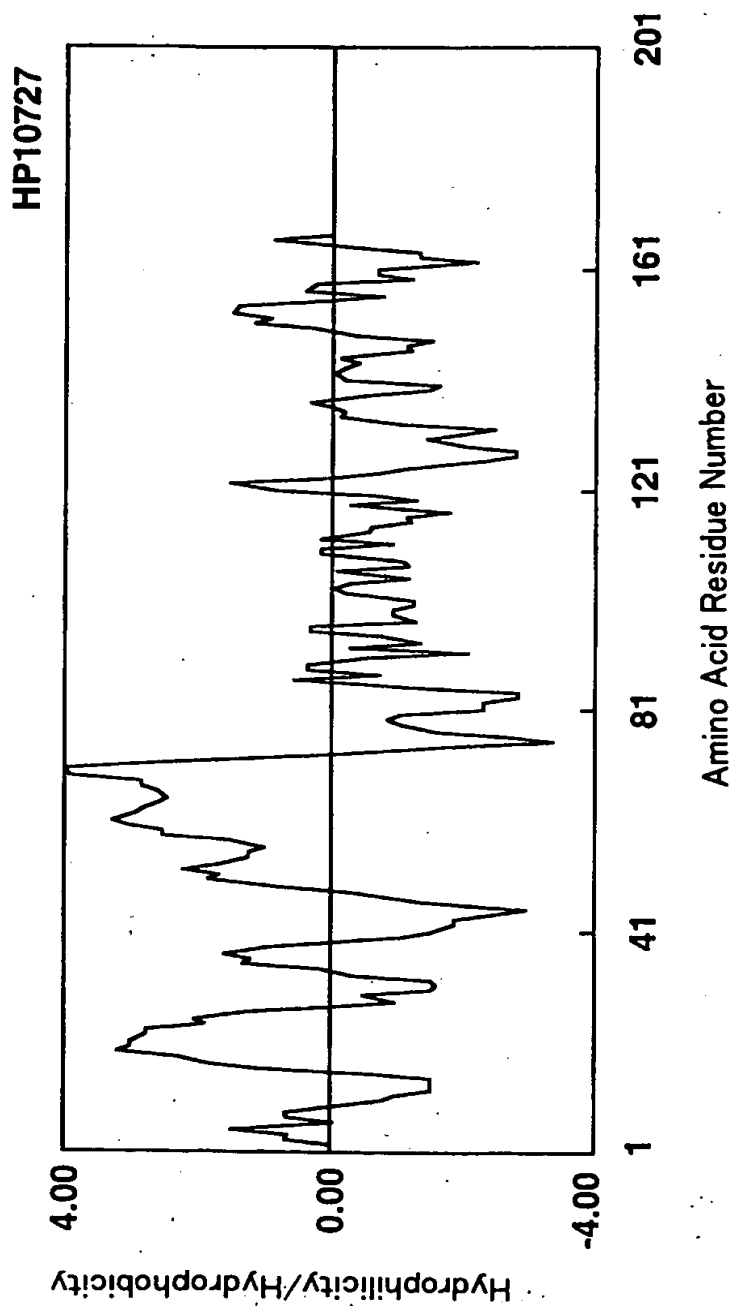


Fig.27

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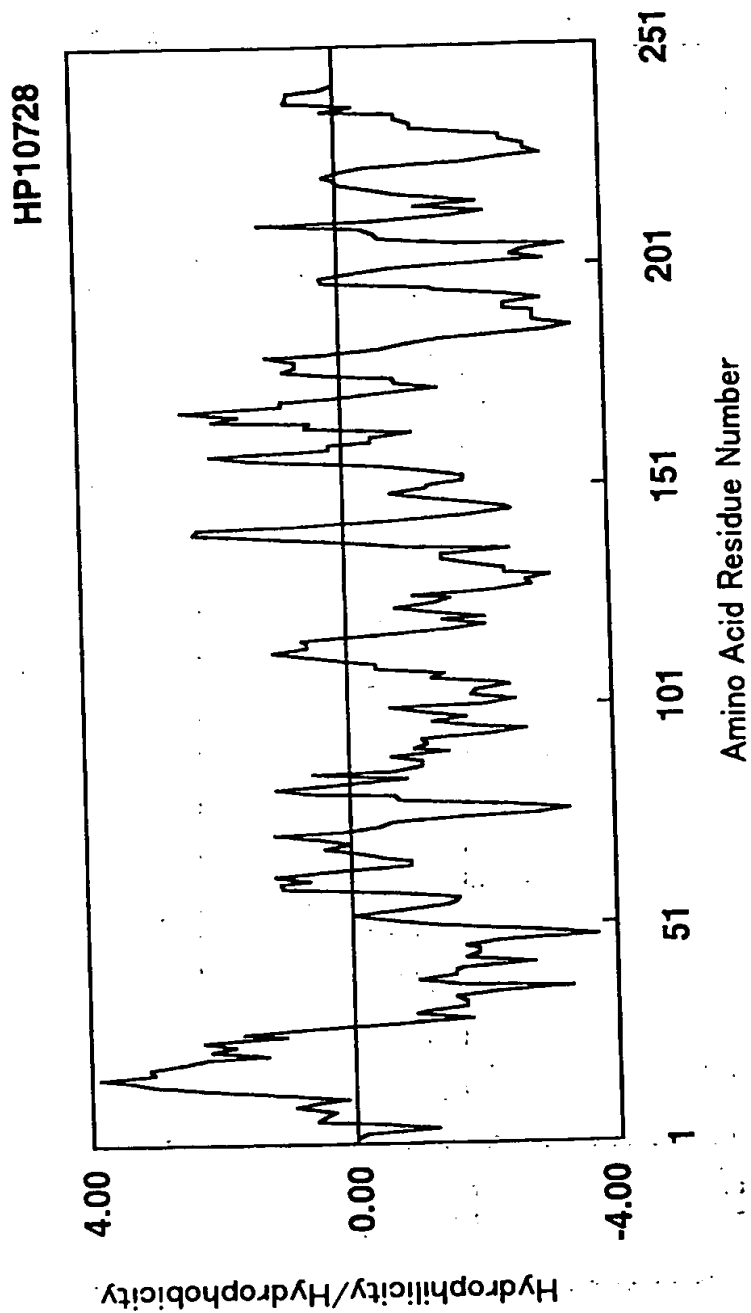


Fig.28

29/50

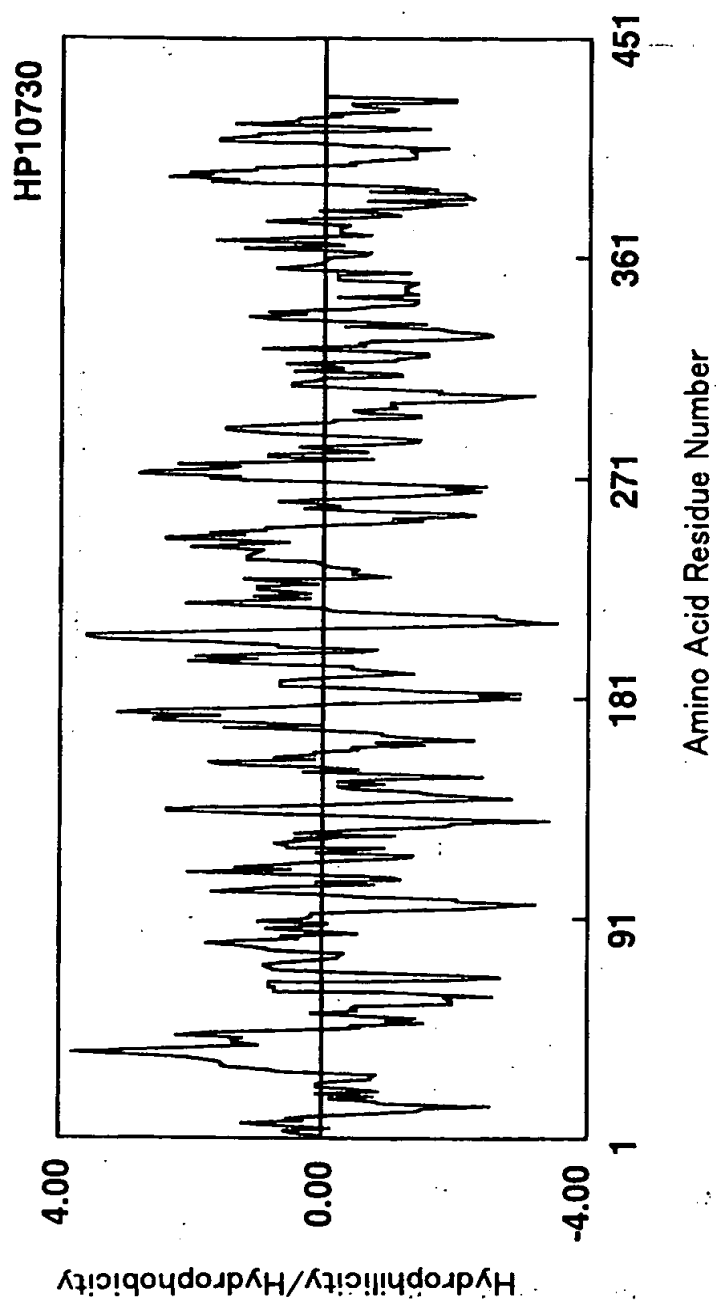


Fig.29

30/50

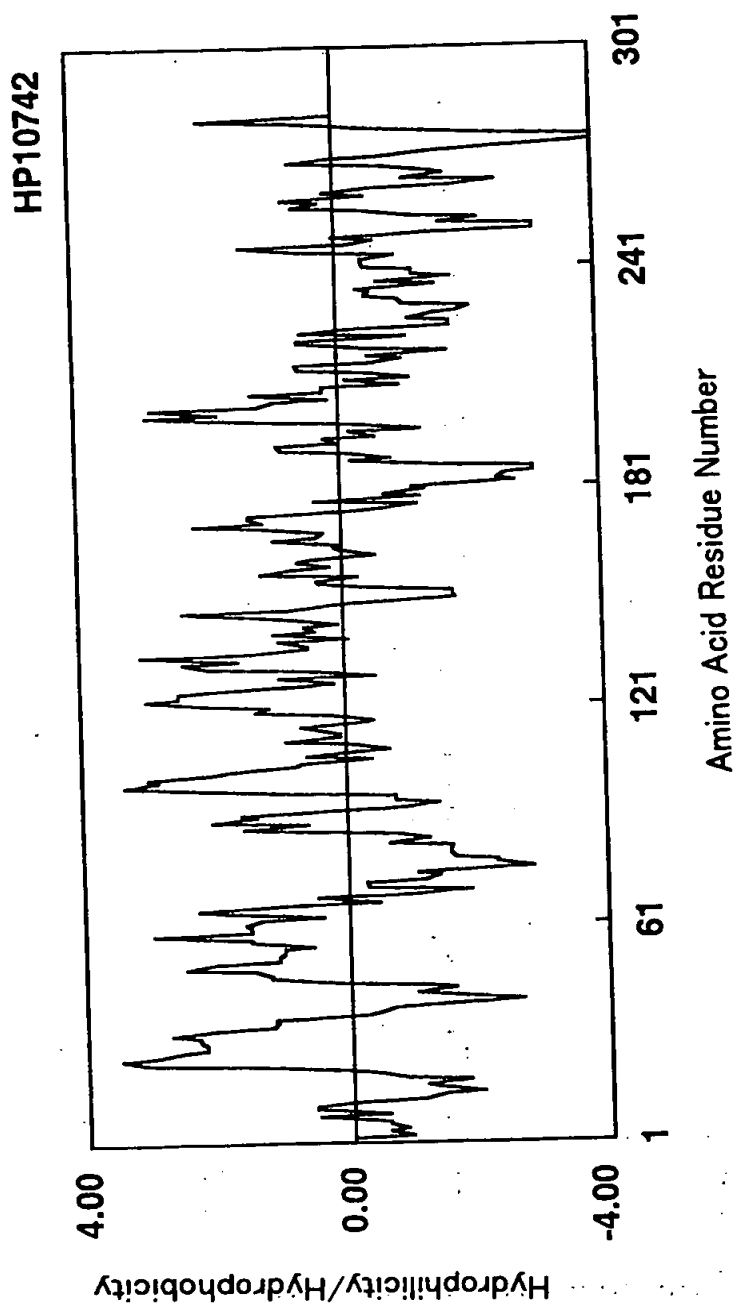


Fig.30

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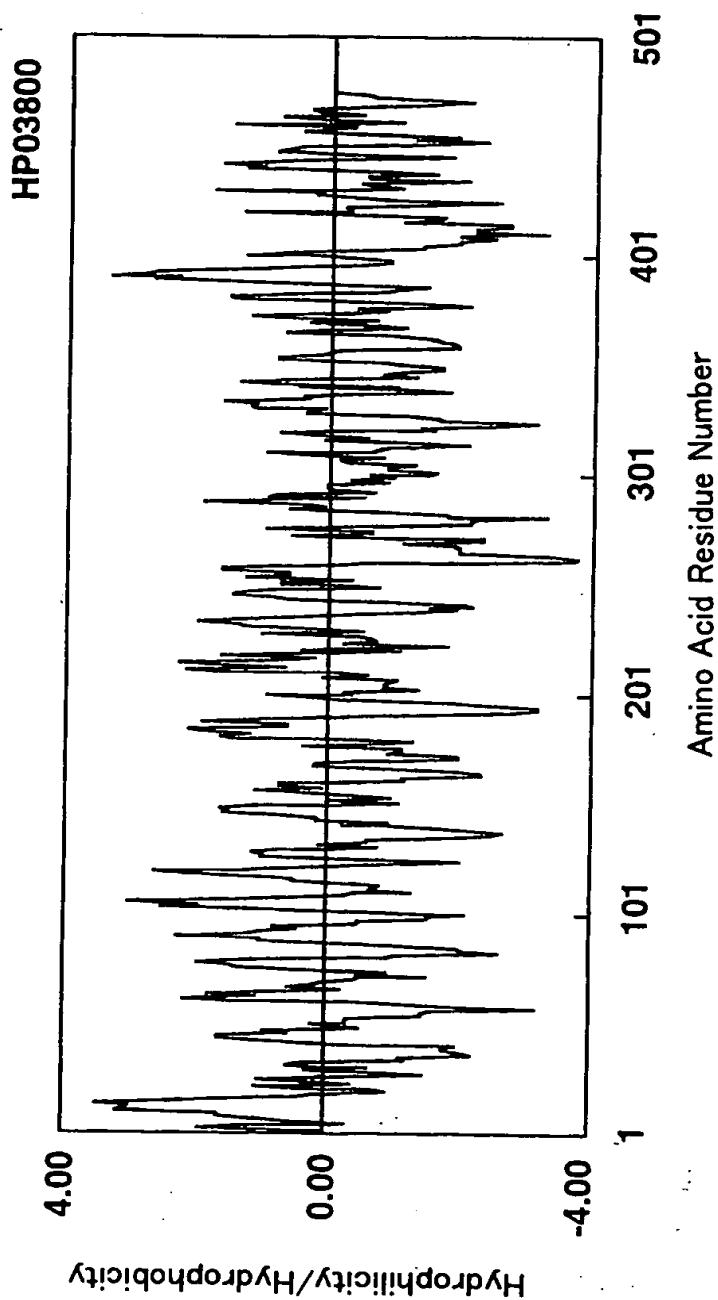


Fig.31

32/50

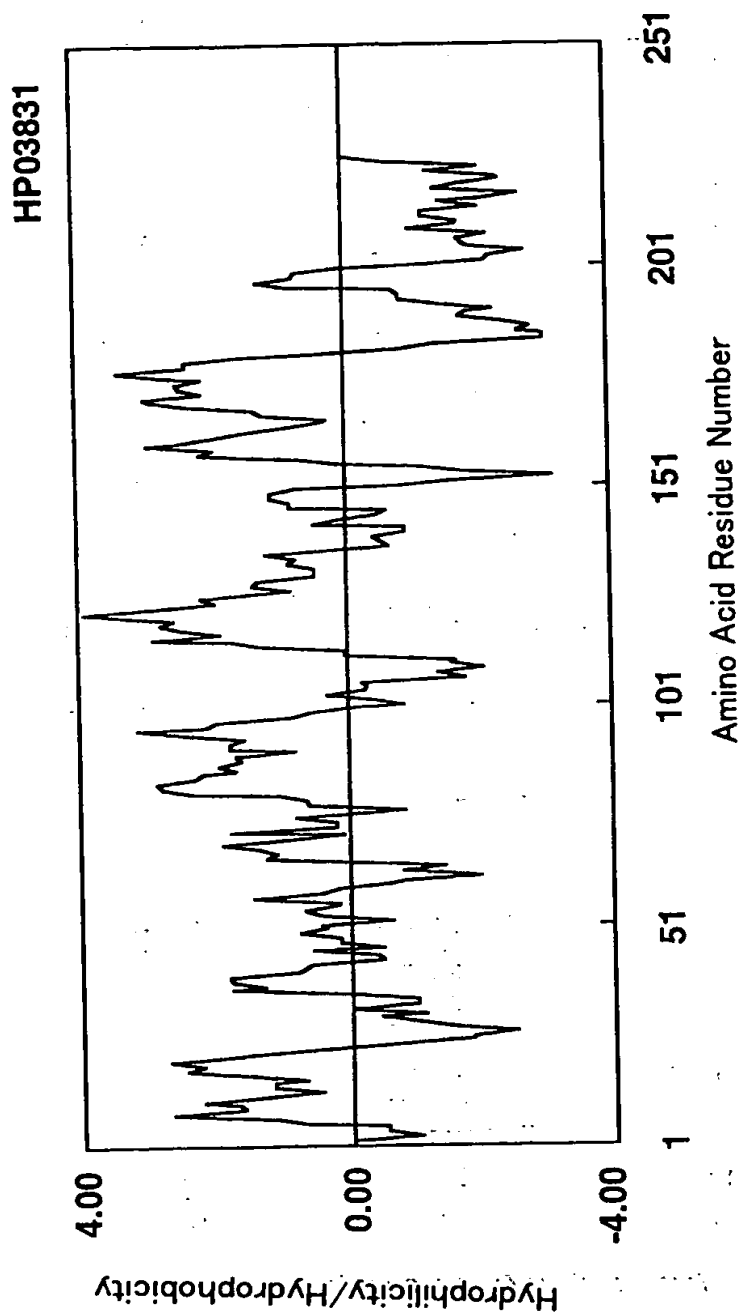


Fig.32

33/50

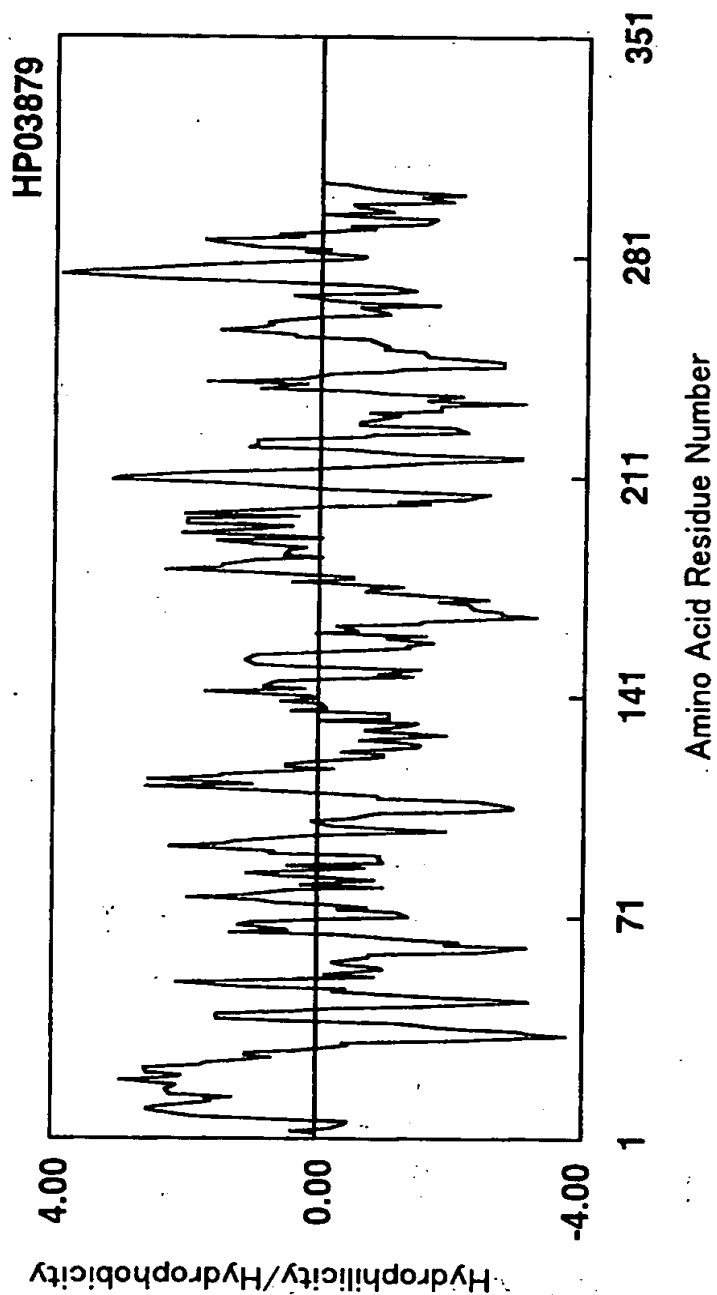


Fig.33

34/50

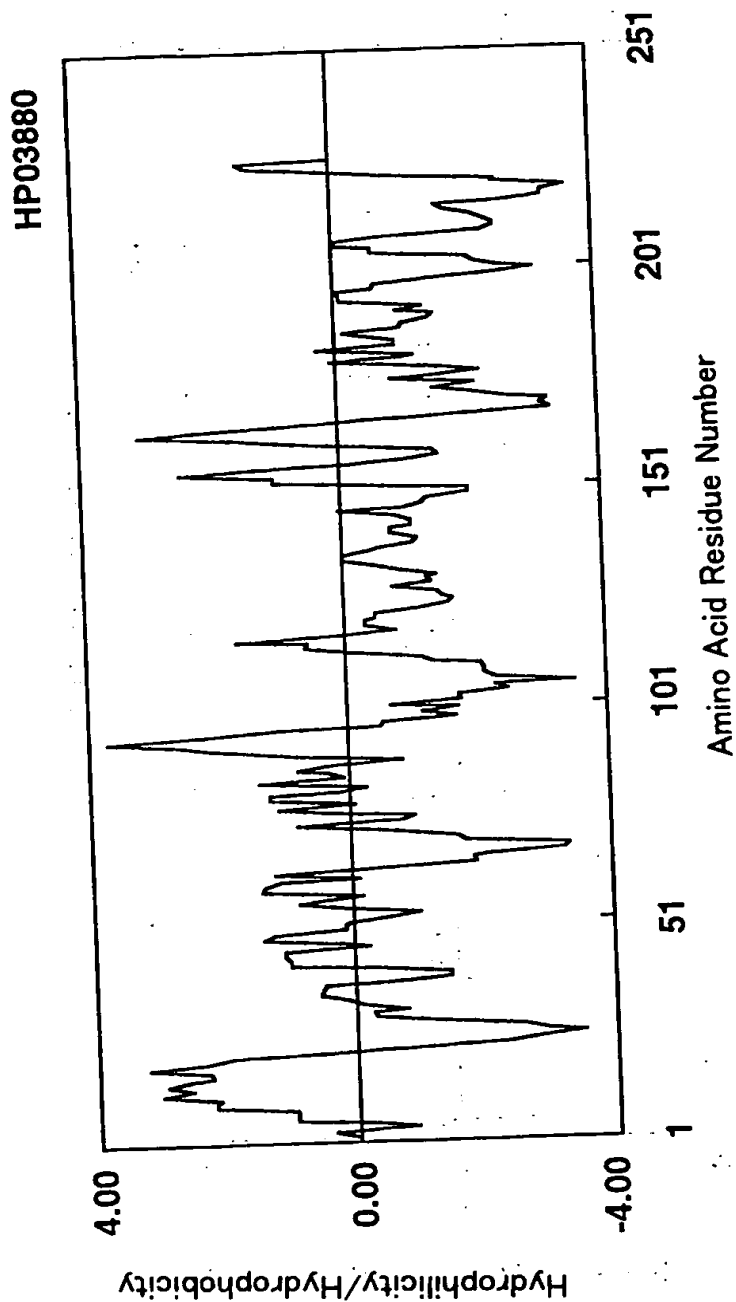


Fig.34

35/50

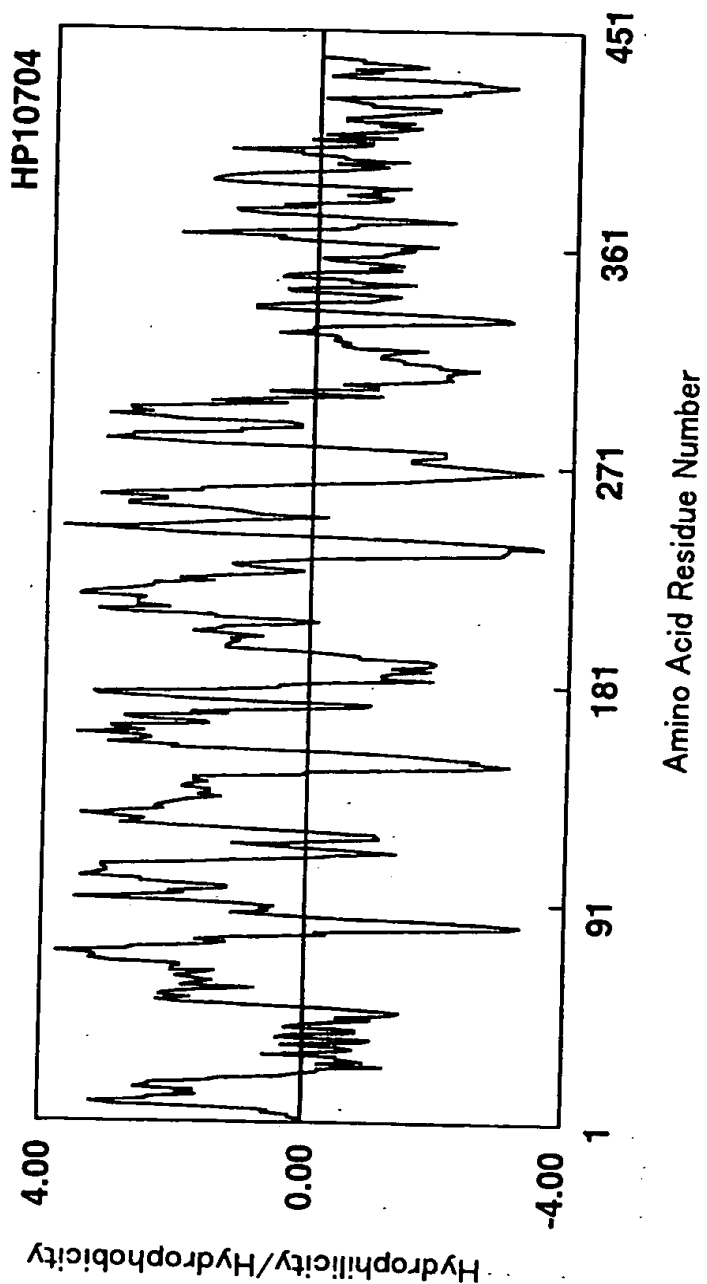


Fig.35

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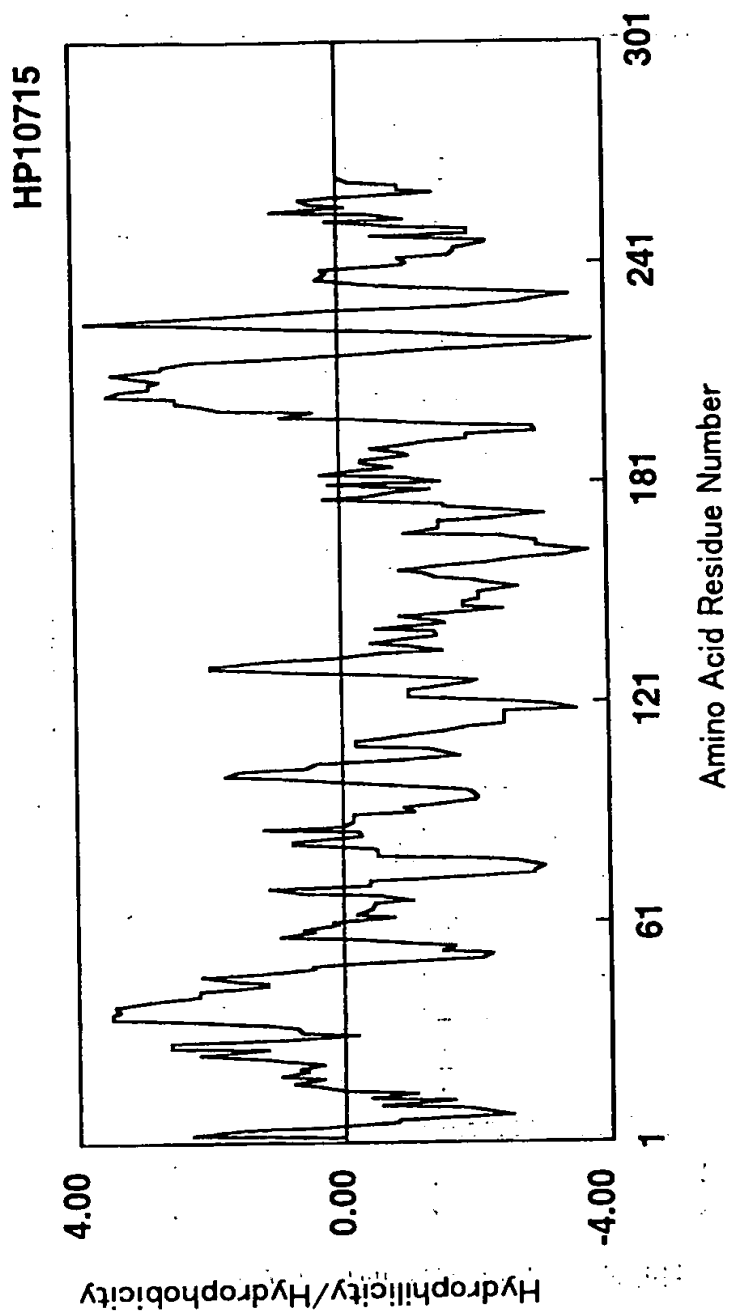


Fig.36

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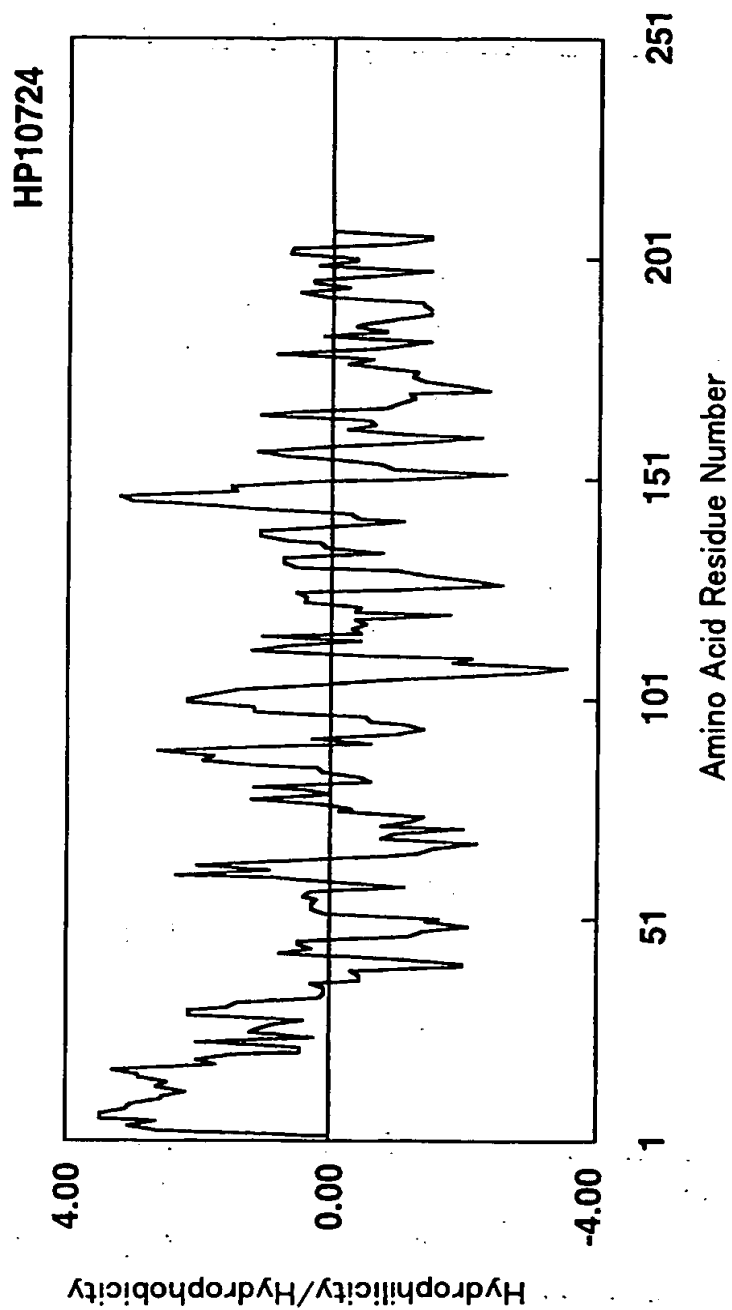


Fig.37

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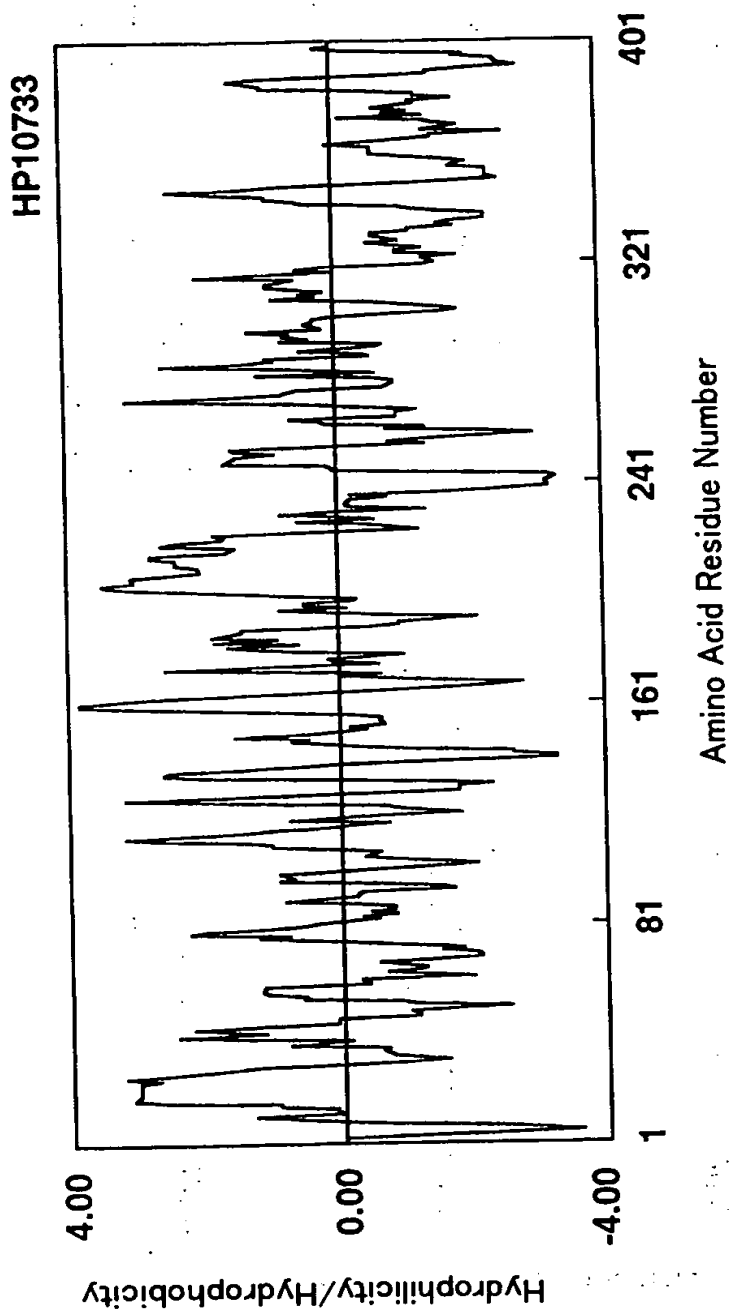


Fig.38

39/50

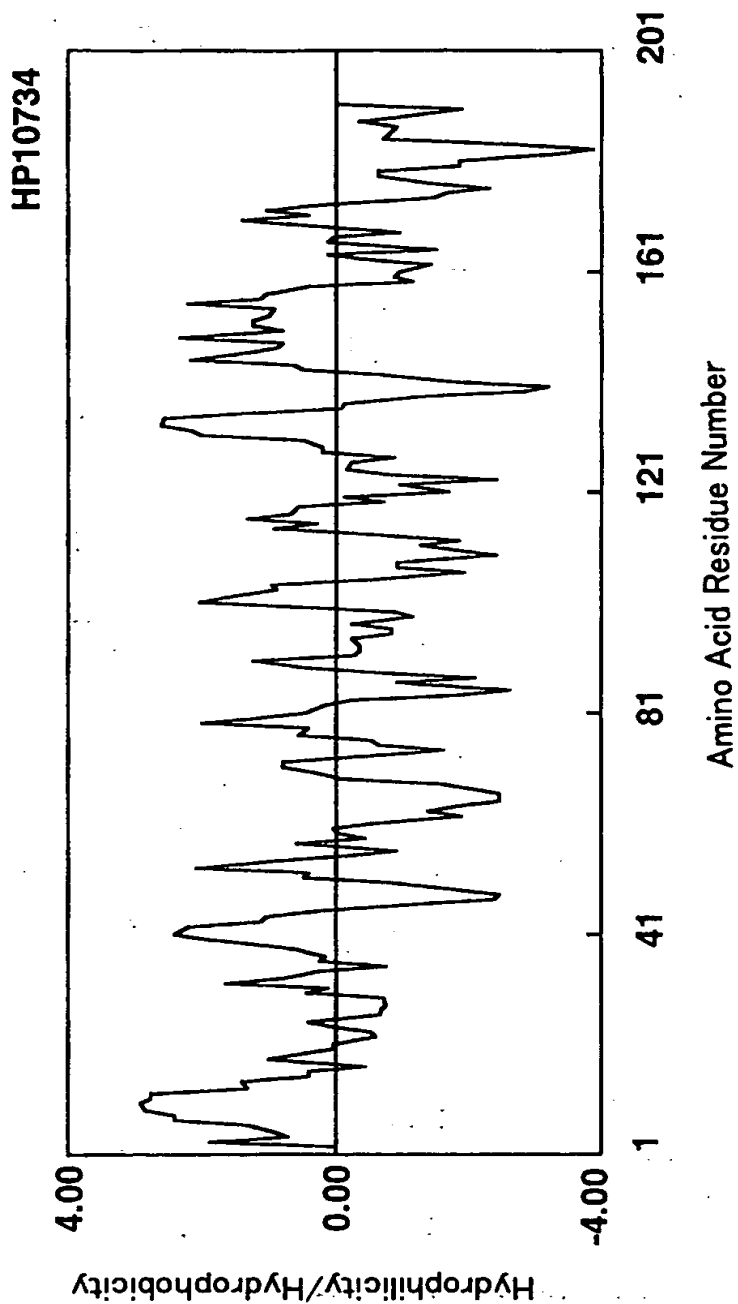


Fig.39

40/50

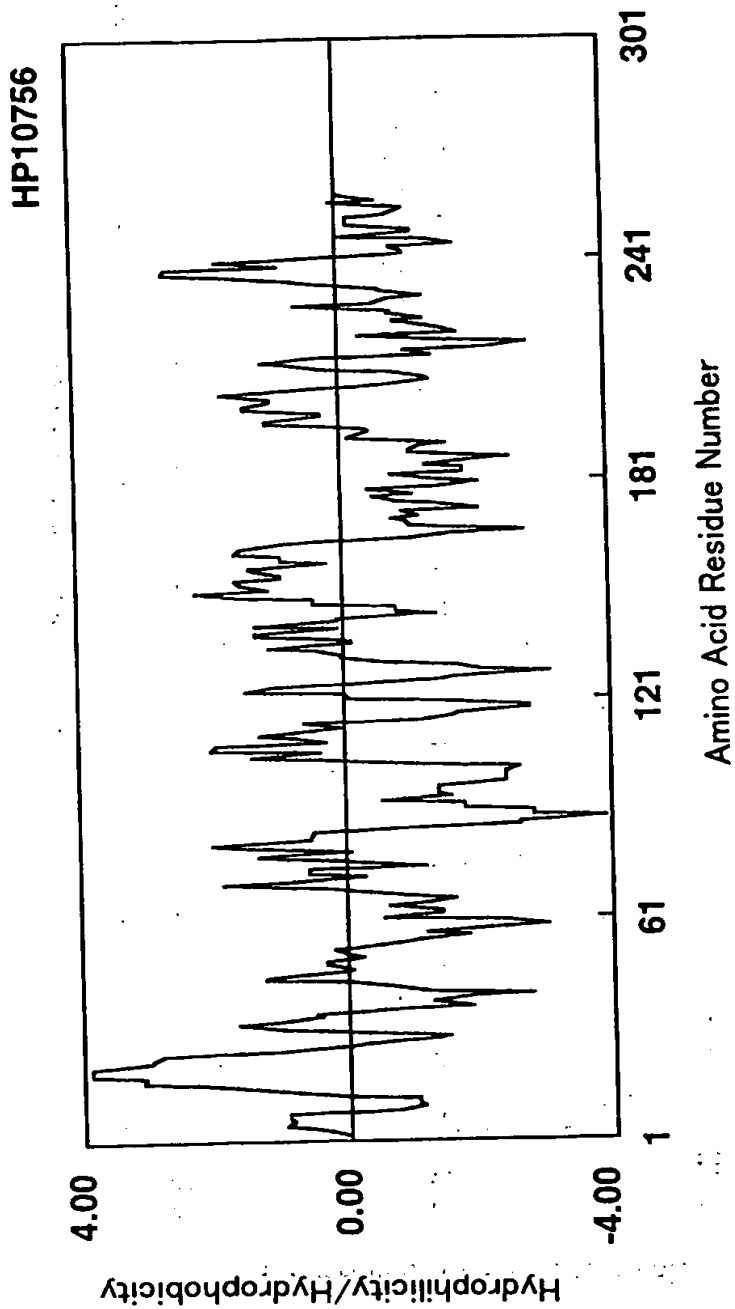


Fig.40

41/50

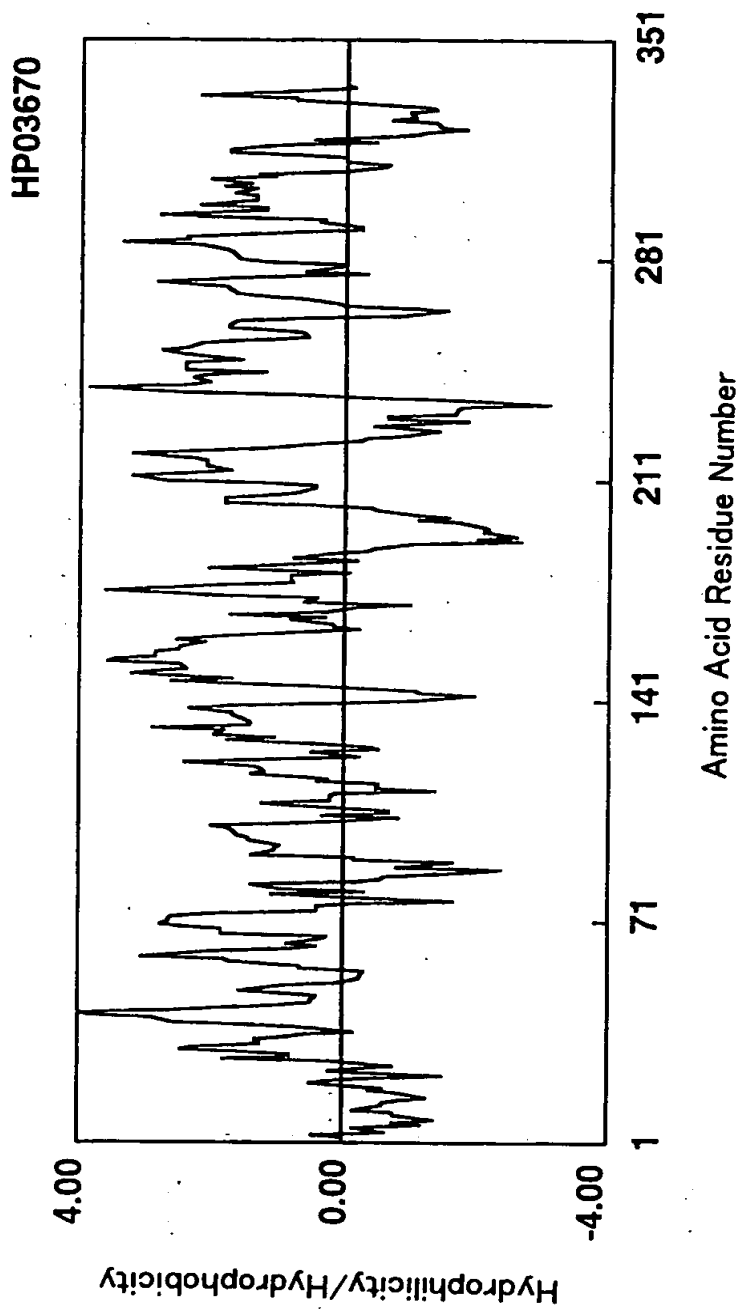


Fig.41

42/50

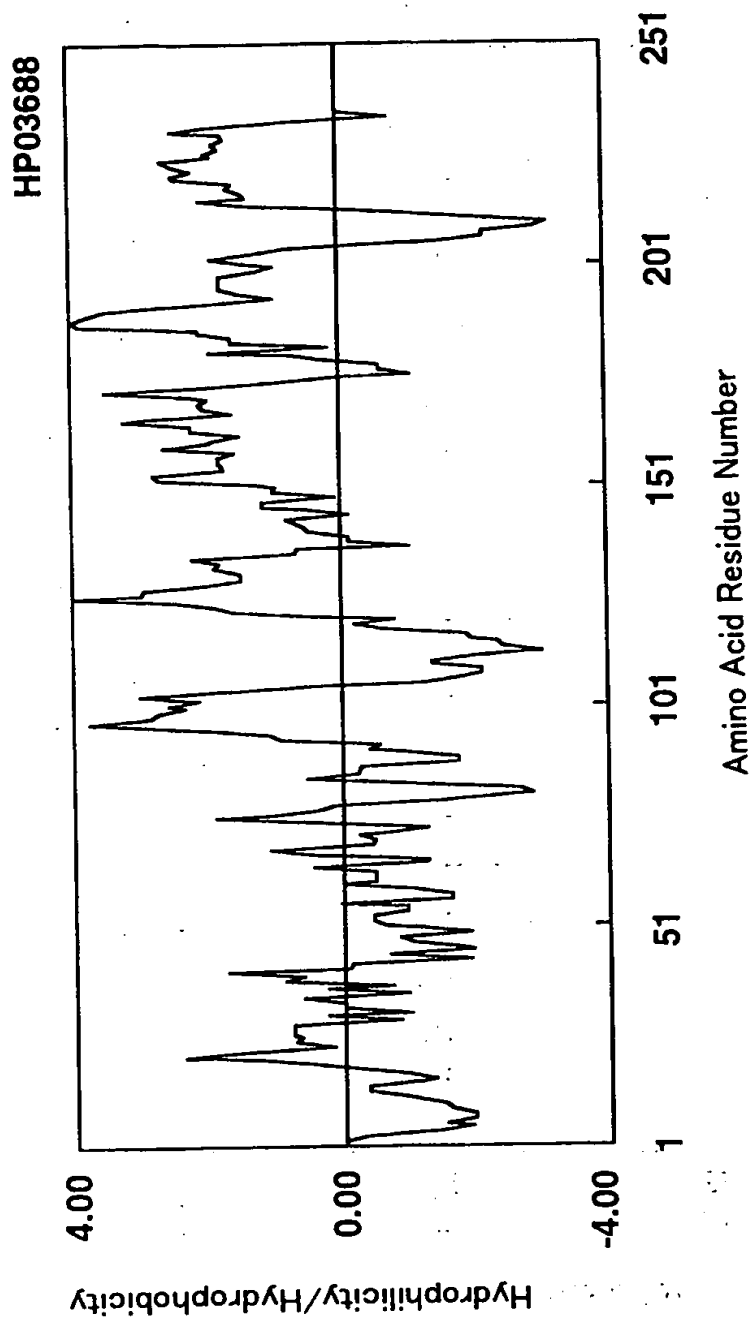


Fig.42

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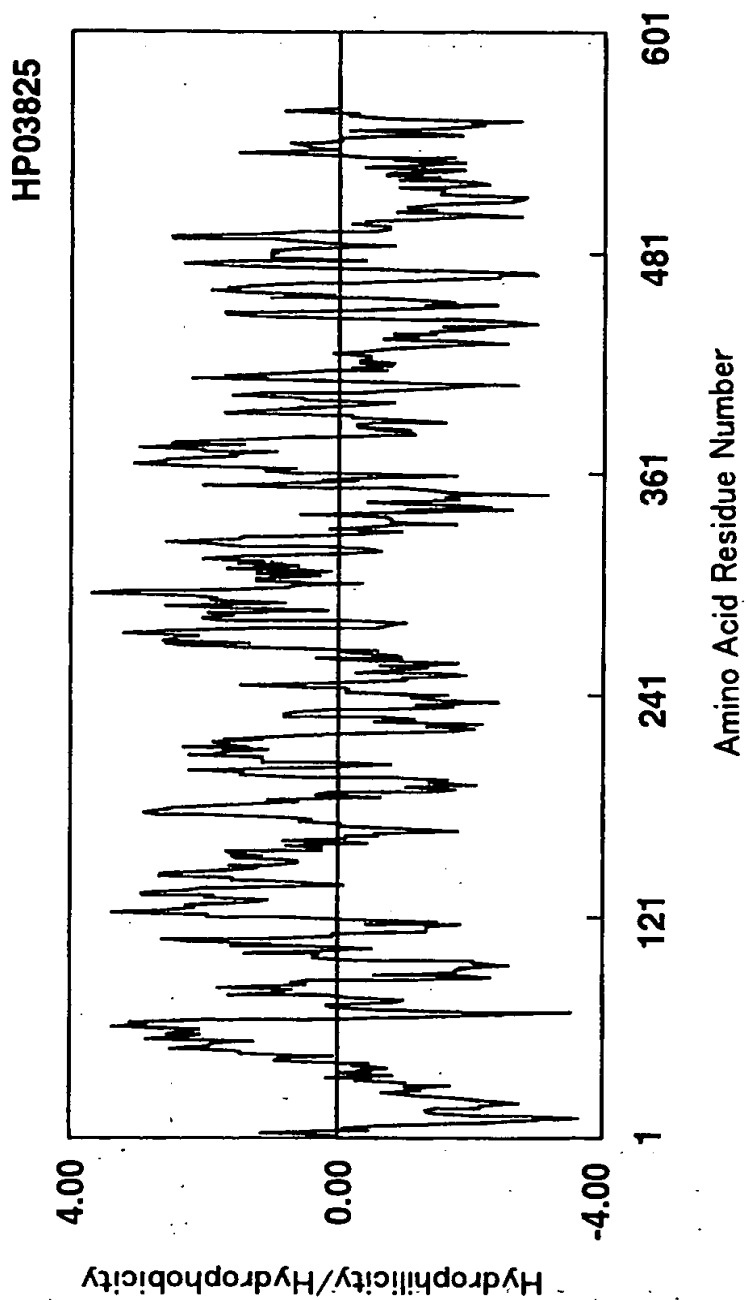


Fig.43

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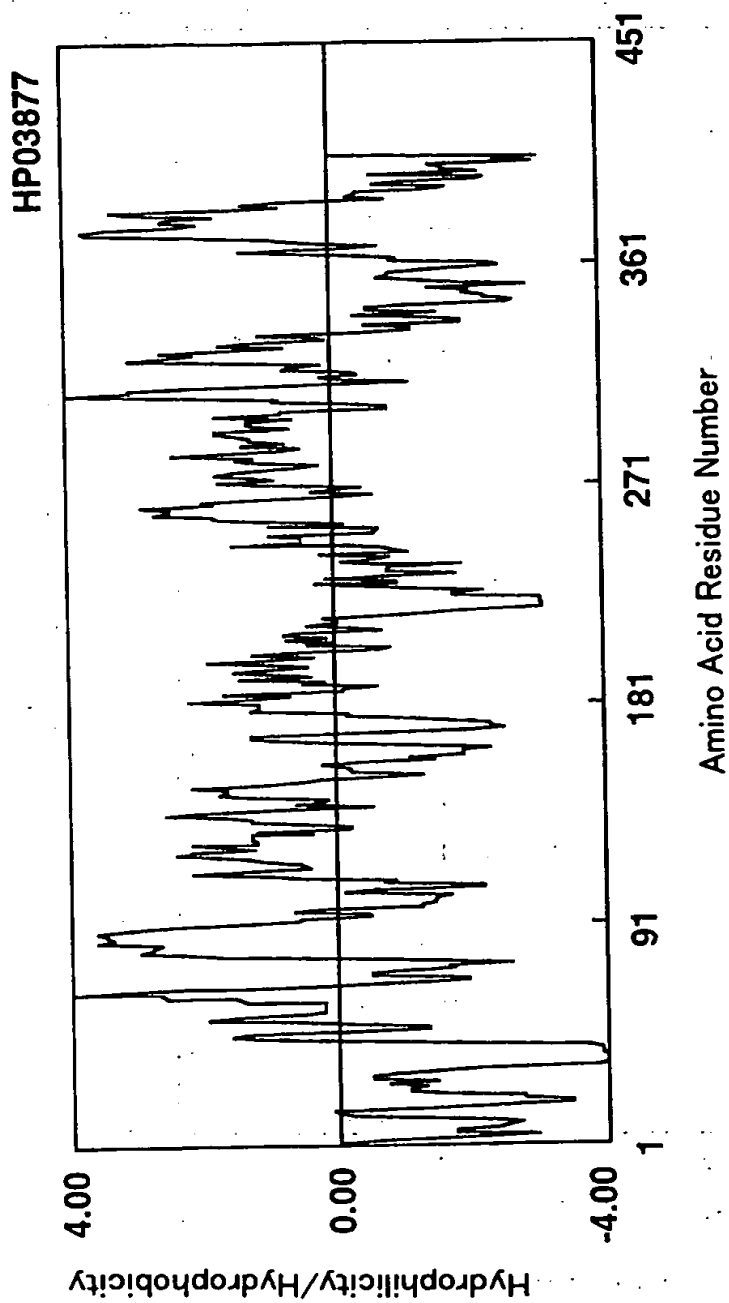


Fig.44

45/50

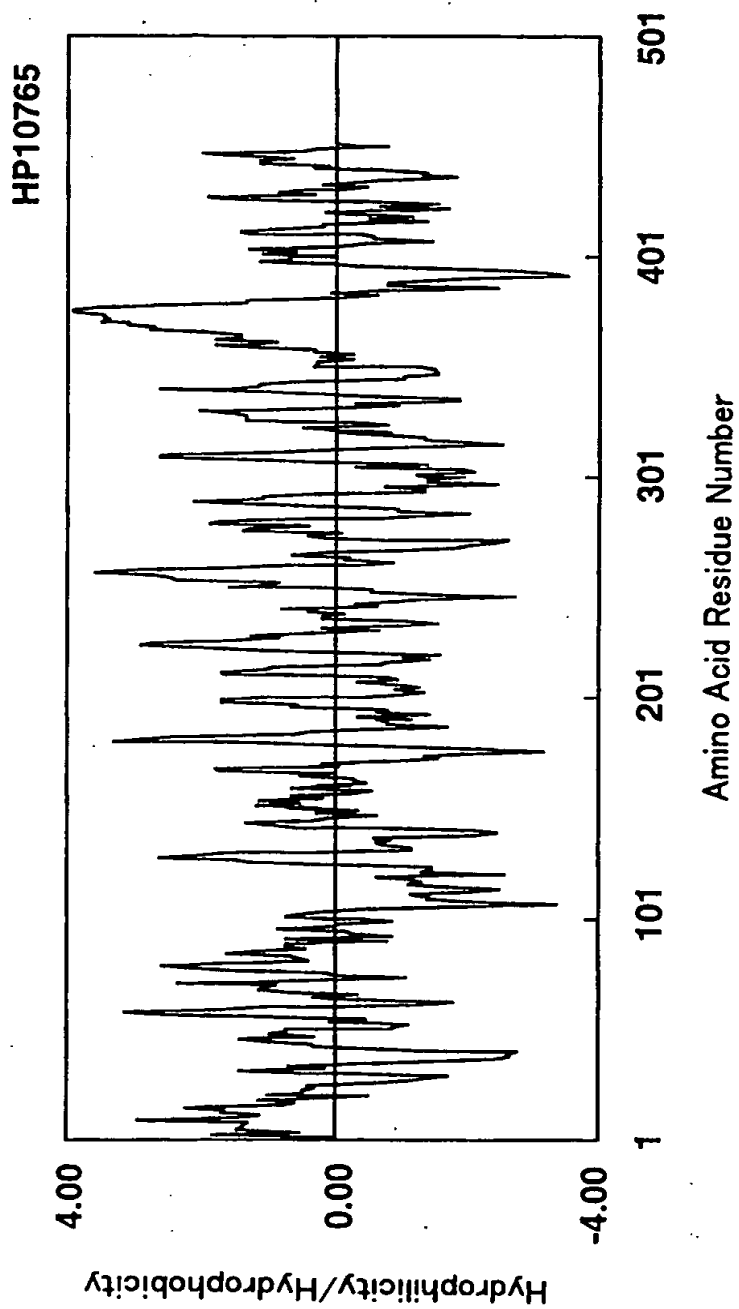


Fig.45

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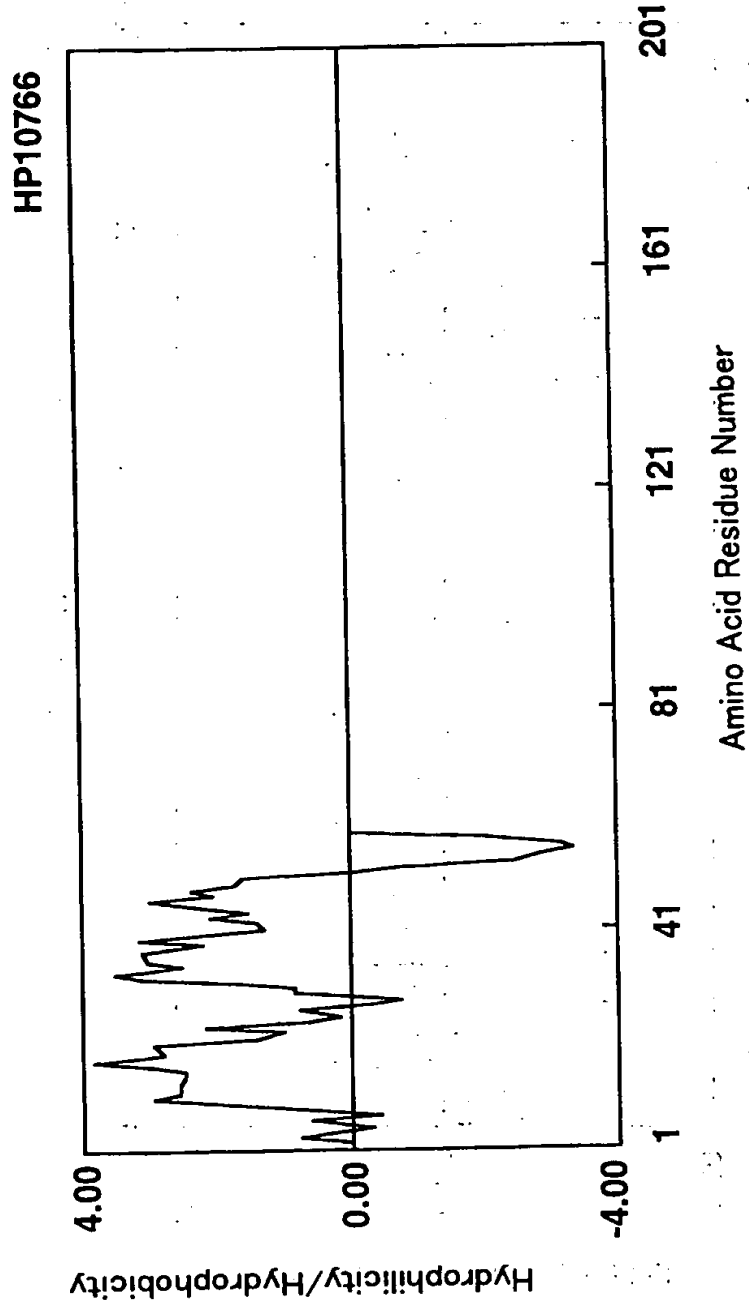


Fig.46

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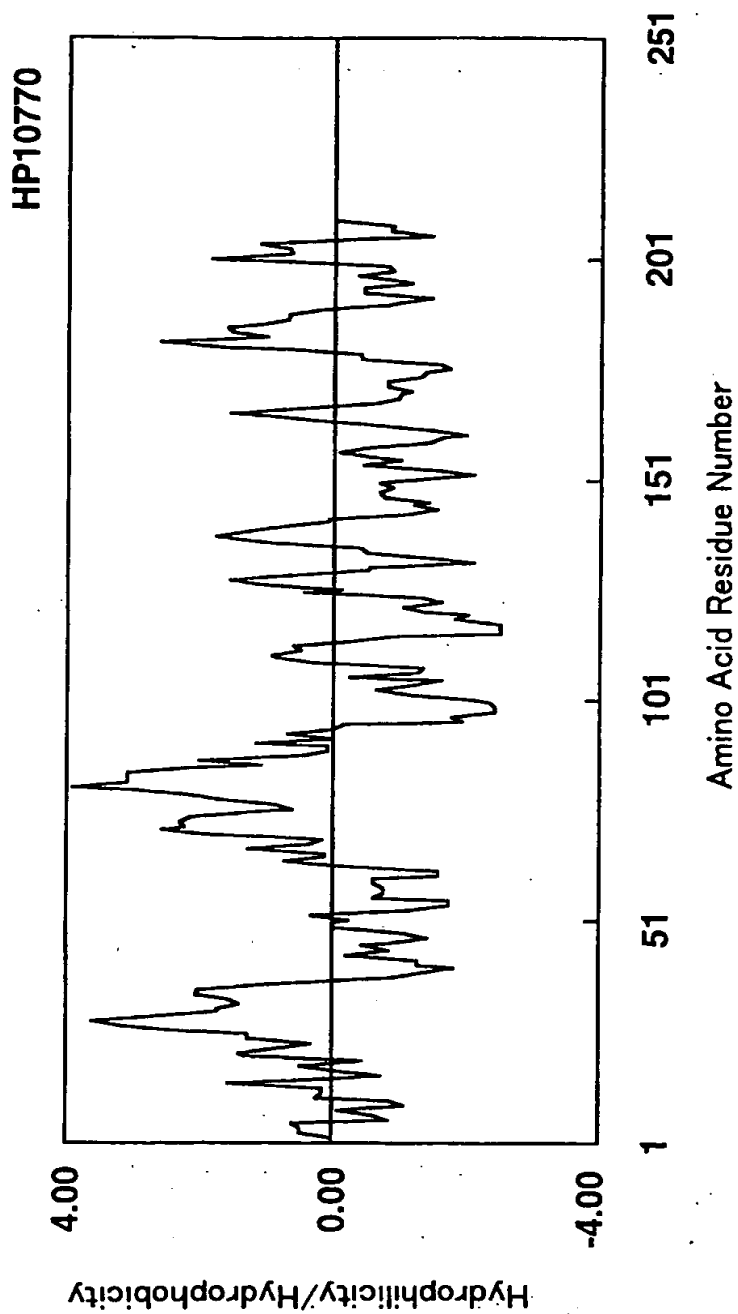


Fig.47

48/50

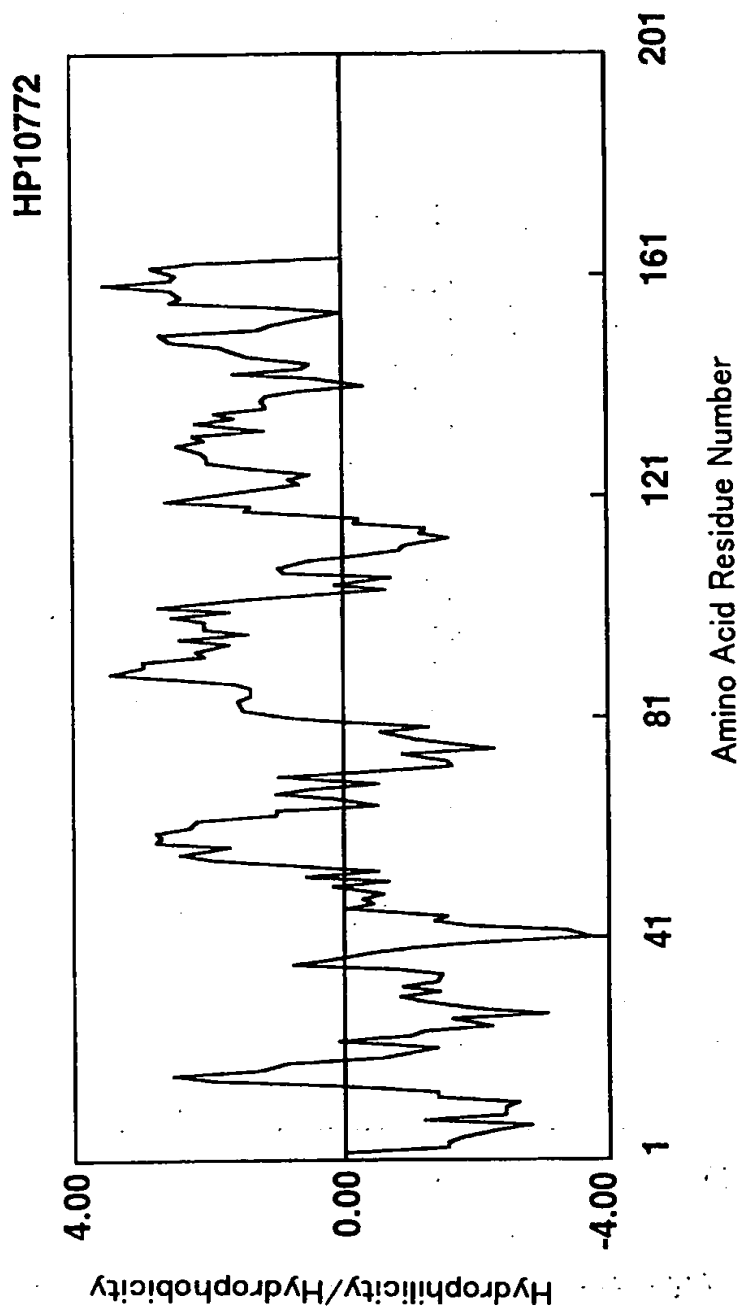


Fig.48

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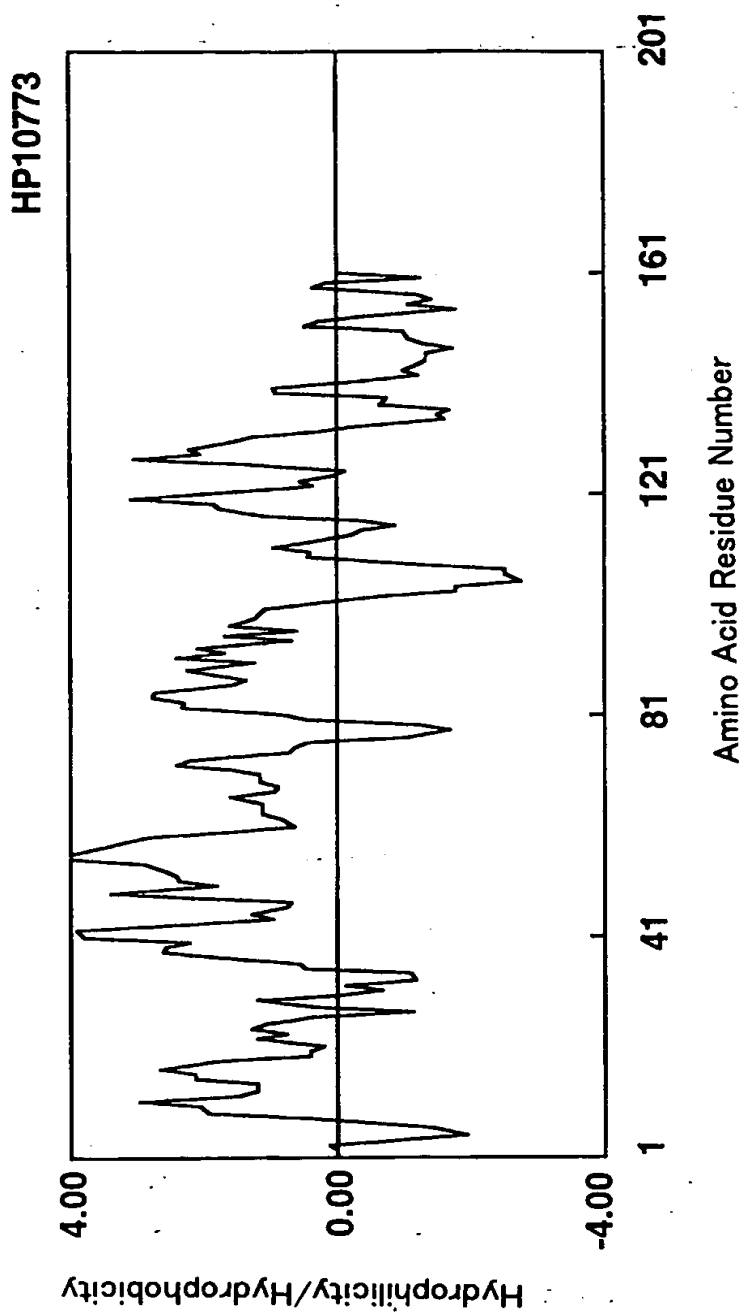


Fig.49

50/50

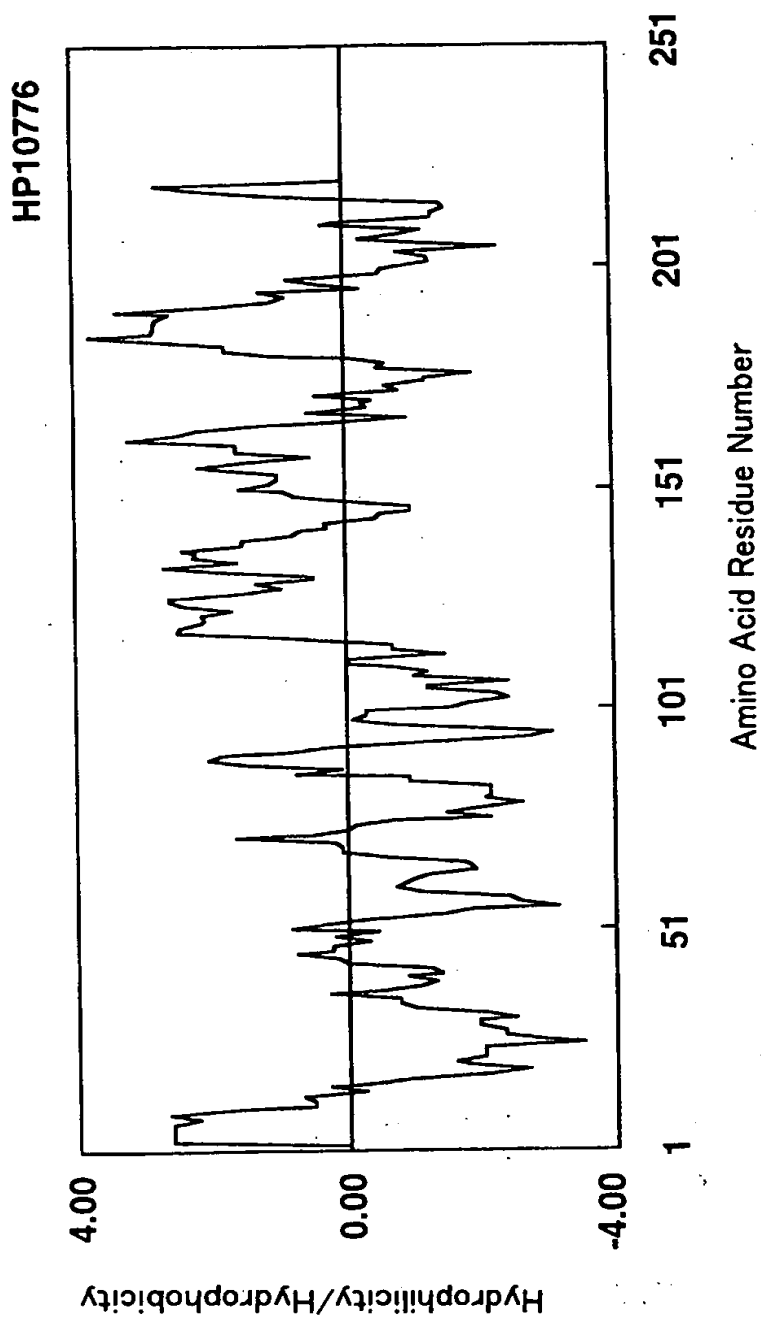


Fig.50

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Protegene Inc.

<120> Human proteins having hydrophobic domains and DNAs encoding these
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<213> Homo sapiens

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Glu Ile Leu Leu Thr Pro Ala Arg Glu Glu Gln Pro Pro Gln His Arg

35 40 45

Ser Lys Arg Gly Ser Ser Val Gly Gly Val Cys Tyr Leu Ser Met Gly

50 55 60

Met Val Val Leu Leu Met Gly Leu Val Phe Ala Ser Val Tyr Ile Tyr

65 70 75 80

Arg Tyr Phe Phe Leu Ala Gln Leu Ala Arg Asp Asn Phe Phe Arg Cys

85 90 95

Gly Val Leu Tyr Glu Asp Ser Leu Ser Ser Gln Val Arg Thr Gln Met

100 105 110

Glu Leu Glu Glu Asp Val Lys Ile Tyr Leu Asp Glu Asn Tyr Glu Arg

115 120 125

Ile Asn Val Pro Val Pro Gln Phe Gly Gly Gly Asp Pro Ala Asp Ile

130 135 140

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Ile His Asp Phe Gln Arg Gly Leu Thr Ala Tyr His Asp Ile Ser Leu

145 150 155 160

Asp Lys Cys Tyr Val Ile Glu Leu Asn Thr Thr Ile Val Leu Pro Pro

165 170 175

Arg Asn Phe Trp Glu Leu Leu Met Asn Val Lys Arg Gly Thr Tyr Leu

180 185 190

Pro Gln Thr Tyr Ile Ile Gln Glu Glu Met Val Val Thr Glu His Val

195 200 205

Ser Asp Lys Glu Ala Leu Gly Ser Phe Ile Tyr His Leu Cys Asn Gly

210 215 220

Lys Asp Thr Tyr Arg Leu Arg Arg Arg Ala Thr Arg Arg Arg Ile Asn

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Lys Arg Gly Ala Lys Asn Cys Asn Ala Ile Arg His Phe Glu Asn Thr

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35 40 45
Gly Ala Pro Leu Thr Phe Arg Ile Asp Arg Gly Arg Tyr Gly Leu Asp
50 55 60
Ser Pro Lys Ala Glu Val Arg Gly Gln Val Leu Ala Pro Leu Pro Leu
65 70 75 80
His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg Phe Phe
85 90 95
Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg Gly Asn
100 105 110
Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn Ala Val
115 120 125
Ala Val Val Ile Tyr Asn Asn Lys Ser Lys Glu Glu Pro Val Thr Met
130 135 140
Thr His Pro Gly Thr Gly Asp Ile Ile Ala Val Met Ile Thr Glu Leu
145 150 155 160
Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val Gln
165 170 175
Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser Arg
180 185 190
Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile Ile
195 200 205
Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr Thr
210 215 220

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Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys Lys

225 230 235 240

Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp Lys Glu

245 250 255

Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser Tyr Lys

260 265 270

Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe His Lys

275 280 285

Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro Met Cys

290 295 300

Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu Pro Cys

305 310 315 320

Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr Gln Ala

325 330 335

Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn Ser Leu

340 345 350

Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro Gln Asp

355 360 365

Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val Thr Lys

370 375 380

Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu Thr Leu

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Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn Glu Val

405 410 415

Glu Trp Phe

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25

30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly

35

40

45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr

50

55

60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu

65

70

75

80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly

85

90

95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro

100

105

110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser

115

120

125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala

130

135

140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg

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 165 170 175
Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
 180 185 190
Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
 195 200 205
Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
 210 215 220
Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
225 230 235 240
Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
 245 250 255
Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
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Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr
 275 280 285
Gly Leu Lys Thr Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
 290 295 300
Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly
305 310 315 320
Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
 325 330 335
Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala
 340 345 350

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Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro

355 360 365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu

370 375 380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys

385 390 395 400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys

405 410 415

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<213> Homo sapiens

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Tyr Ala Lys Ala Ser Asp Leu Tyr Ile Thr Leu Pro Leu Ala Leu Leu

35 40 45

Phe Leu Ile Val Arg Tyr Phe Phe Glu Leu Tyr Val Ala Thr Pro Leu

50 55 60

Ala Ala Leu Leu Asn Ile Lys Glu Lys Thr Arg Leu Arg Ala Pro Pro

65 70 75 80

Asn Ala Thr Leu Glu His Phe Tyr Leu Thr Ser Gly Lys Gln Pro Lys

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	85		90		95
Gln Val Glu Val Glu Leu Leu Ser Arg Gln Ser Gly Leu Ser Gly Arg					
100		105		110	
Gln Val Glu Arg Trp Phe Arg Arg Arg Arg Asn Gln Asp Arg Pro Ser					
115		120		125	
Leu Leu Lys Lys Phe Arg Glu Ala Ser Trp Arg Phe Thr Phe Tyr Leu					
130		135		140	
Ile Ala Phe Ile Ala Gly Met Ala Val Ile Val Asp Lys Pro Trp Phe					
145		150		155	160
Tyr Asp Met Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile					
165		170		175	
Pro Ser Gln Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser					
180		185		190	
Leu Leu Phe Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu					
195		200		205	
Gln Ile Ile His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp					
210		215		220	
Phe Ala Asn Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp					
225		230		235	240
Ser Ser Asp Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly					
245		250		255	
Trp Lys Asn Thr Cys Asn Asn Ile Phe Ile Val Phe Ala Ile Val Phe					
260		265		270	
Ile Ile Thr Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys Thr					
275		280		285	

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Leu Val Tyr Pro Leu Glu Leu Tyr Pro Ala Phe Phe Gly Tyr Tyr Phe

290 295 300

Phe Asn Ser Met Met Gly Val Leu Gln Leu Leu His Ile Phe Trp Ala

305 310 315 320

Tyr Leu Ile Leu Arg Met Ala His Lys Phe Ile Thr Gly Lys Leu Val

325 330 335

Glu Asp Glu Arg Ser Asp Arg Glu Glu Thr Glu Ser Ser Glu Gly Glu

340 345 350

Glu Ala Ala Ala Gly Gly Gly Ala Lys Ser Arg Pro Leu Ala Asn Gly

355 360 365

His Pro Ile Leu Asn Asn Asn His Arg Lys Asn Asp

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20 25 30

Ala Ile Thr Leu Arg Arg Pro Gly Cys Glu Leu Glu Ala Cys Ser Pro

35 40 45

Asp Ala Asp Met Leu Asp Tyr Leu Leu Ser Leu Gly Gln Ile Ser Arg

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50	55	60	
Arg Asp Ala Leu Glu Val Thr Trp Tyr His Ala Ala Asn Ser Lys Lys			
65	70	75	80
Ala Met Thr Ala Ala Leu Asn Ser Asn Ile Thr Val Leu Glu Ala Asp			
85	90	95	
Val Asn Val Glu Gly Leu Gly Thr Ala Asn Glu Thr Gly Val Pro Ile			
100	105	110	
Met Ala His Pro Pro Thr Ile Tyr Ser Asp Asn Thr Leu Glu Gln Trp			
115	120	125	
Leu Asp Ala Val Leu Gly Ser Ser Gln Lys Gly Ile Lys Leu Asp Phe			
130	135	140	
Lys Asn Ile Lys Ala Val Gly Pro Ser Leu Asp Leu Leu Arg Gln Leu			
145	150	155	160
Thr Glu Glu Gly Lys Val Arg Arg Pro Ile Trp Ile Asn Ala Asp Ile			
165	170	175	
Leu Lys Gly Pro Asn Met Leu Ile Ser Thr Glu Val Asn Ala Thr Gln			
180	185	190	
Phe Leu Ala Leu Val Gln Glu Lys Tyr Pro Lys Ala Thr Leu Ser Pro			
195	200	205	
Gly Trp Thr Thr Phe Tyr Met Ser Thr Ser Pro Asn Arg Thr Tyr Thr			
210	215	220	
Gln Ala Met Val Glu Lys Met His Glu Leu Val Gly Gly Val Pro Gln			
225	230	235	240
Arg Val Thr Phe Pro Val Arg Ser Ser Met Val Arg Ala Ala Trp Pro			
245	250	255	

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His Phe Ser Trp Leu Leu Ser Gln Ser Glu Arg Tyr Ser Leu Thr Leu

260

265

270

Trp Gln Ala Ala Ser Asp Pro Met Ser Val Glu Asp Leu Leu Tyr Val

275

280

285

Arg Asp Asn Thr Ala Val His Gln Val Tyr Tyr Asp Ile Phe Glu Pro

290

295

300

Leu Leu Ser Gln Phe Lys Gln Leu Ala Leu Asn Ala Thr Arg Lys Pro

305

310

315

320

Met Tyr Tyr Thr Gly Gly Ser Leu Ile Pro Leu Leu Gln Leu Pro Gly

325

330

335

Asp Asp Gly Leu Asn Val Glu Trp Leu Val Pro Asp Val Gln Gly Ser

340

345

350

Gly Lys Thr Ala Thr Met Thr Leu Pro Asp Thr Glu Gly Met Ile Leu

355

360

365

Leu Asn Thr Gly Leu Glu Gly Thr Val Ala Glu Asn Pro Val Pro Ile

370

375

380

Val His Thr Pro Ser Gly Asn Ile Leu Thr Leu Glu Ser Cys Leu Gln

385

390

395

400

Gln Leu Ala Thr His Pro Gly His Trp Gly Ile His Leu Gln Ile Ala

405

410

415

Glu Pro Ala Ala Leu Arg Pro Ser Leu Ala Leu Leu Ala Arg Leu Ser

420

425

430

Ser Leu Gly Leu Leu His Trp Pro Val Trp Val Gly Ala Lys Ile Ser

435

440

445

His Gly Ser Phe Ser Val Pro Gly His Val Ala Gly Arg Glu Leu Leu

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Thr Ala Val Ala Glu Val Phe Pro His Val Thr Val Ala Pro Gly Trp
465 470 475 480
Pro Glu Glu Val Leu Gly Ser Gly Tyr Arg Glu Gln Leu Leu Thr Asp
 485 490 495
Met Leu Glu Leu Cys Gln Gly Leu Trp Gln Pro Val Ser Phe Gln Met
 500 505 510
Gln Ala Met Leu Leu Gly His Ser Thr Ala Gly Ala Ile Gly Arg Leu
 515 520 525
Leu Ala Ser Ser Pro Arg Ala Thr Val Thr Val Glu His Asn Pro Ala
 530 535 540
Gly Gly Asp Tyr Ala Ser Val Arg Thr Ala Leu Leu Ala Ala Arg Ala
545 550 555 560
Val Asp Arg Thr Arg Val Tyr Tyr Arg Leu Pro Gln Gly Tyr His Lys
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Asp Leu Leu Ala His Val Gly Arg Asn
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<213> Homo sapiens

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20

25

30

Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu

35

40

45

Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg

50

55

60

Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn

65

70

75

80

Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val

85

90

95

Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His

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Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp

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120

125

Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg

130

135

140

Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Arg Glu Ala

145

150

155

160

Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys

165

170

175

Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu

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185

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Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu

195

200

205

Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu

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210 215 220
Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg
225 230 235 240
Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu
245 250 255
Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser
260 265 270
Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys
275 280 285
Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe
290 295 300
Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr
305 310 315 320
Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
325 330

<210> 7

<211> 345

<212> PRT

<213> Homo sapiens

<400> 7

Met Ser Pro Glu Glu Trp Thr Tyr Leu Val Val Leu Leu Ile Ser Ile

1 5 10 15

Pro Ile Gly Phe Leu Phe Lys Lys Ala Gly Pro Gly Leu Lys Arg Trp

20 25 30

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Gly Ala Ala Ala Val Gly Leu Gly Leu Thr Leu Phe Thr Cys Gly Pro

35

40

45

His Thr Leu His Ser Leu Val Thr Ile Leu Gly Thr Trp Ala Leu Ile

50

55

60

Gln Ala Gln Pro Cys Ser Cys His Ala Leu Ala Leu Ala Trp Thr Phe

65

70

75

80

Ser Tyr Leu Leu Phe Phe Arg Ala Leu Ser Leu Leu Gly Leu Pro Thr

85

90

95

Pro Thr Pro Phe Thr Asn Ala Val Gln Leu Leu Leu Thr Leu Lys Leu

100

105

110

Val Ser Leu Ala Ser Glu Val Gln Asp Leu His Leu Ala Gln Arg Lys

115

120

125

Glu Met Ala Ser Gly Phe Ser Lys Gly Pro Thr Leu Gly Leu Leu Pro

130

135

140

Asp Val Pro Ser Leu Met Glu Thr Leu Ser Tyr Ser Tyr Cys Tyr Val

145

150

155

160

Gly Ile Met Thr Gly Pro Phe Phe Arg Tyr Arg Thr Tyr Leu Asp Trp

165

170

175

Leu Glu Gln Pro Phe Pro Gly Ala Val Pro Ser Leu Arg Pro Leu Leu

180

185

190

Arg Arg Ala Trp Pro Ala Pro Leu Phe Gly Leu Leu Phe Leu Leu Ser

195

200

205

Ser His Leu Phe Pro Leu Glu Ala Val Arg Glu Asp Ala Phe Tyr Ala

210

215

220

Arg Pro Leu Pro Ala Arg Leu Phe Tyr Met Ile Pro Val Phe Phe Ala

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225 230 235 240
Phe Arg Met Arg Phe Tyr Val Ala Trp Ile Ala Ala Glu Cys Gly Cys
 245 250 255
Ile Ala Ala Gly Phe Gly Ala Tyr Pro Val Ala Ala Lys Ala Arg Ala
 260 265 270
Gly Gly Gly Pro Thr Leu Gln Cys Pro Pro Pro Ser Ser Pro Glu Lys
 275 280 285
Ala Ala Ser Leu Glu Tyr Asp Tyr Glu Thr Ile Arg Asn Ile Asp Cys
 290 295 300
Tyr Ser Thr Asp Phe Cys Val Arg Val Arg Asp Gly Met Arg Tyr Trp
305 310 315 320
Asn Met Thr Val Gln Trp Trp Leu Ala Gln Tyr Ile Tyr Lys Ser Ala
 325 330 335
Pro Ala Arg Ser Tyr Val Leu Arg Leu
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<211> 89

<212> PRT

<213> Homo sapiens

<400> 8

Met Tyr Met Gln Asp Tyr Trp Arg Thr Trp Leu Lys Gly Leu Arg Gly

1

5

10

15

Phe Phe Phe Val Gly Val Leu Phe Ser Ala Val Ser Ile Ala Ala Phe

20

25

30

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Cys Thr Phe Leu Val Leu Ala Ile Thr Arg His Gln Ser Leu Thr Asp

35

40

45

Pro Thr Ser Tyr Tyr Leu Ser Ser Val Trp Ser Phe Ile Ser Phe Lys

50

55

60

Trp Ala Phe Leu Leu Ser Leu Tyr Ala His Arg Tyr Arg Ala Asp Phe

65

70

75

80

Ala Asp Ile Ser Ile Leu Ser Asp Phe

85

<210> 9

<211> 406

<212> PRT

<213> Homo sapiens

<400> 9

Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly His Cys Ala Pro

1

5

10

15

Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly

20

25

30

Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn

35

40

45

Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr

50

55

60

Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val

65

70

75

80

Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu Ser Val Asn Trp

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85	90	95
Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu Met Val Leu Pro		
100	105	110
Lys Asp Ser Ile Gln Phe Ser Ser Ala Leu Val Phe Thr Arg Leu Leu		
115	120	125
Glu Phe Asp Ser Thr Asn Val Ser Asp Thr Ala Ala Lys Pro Leu Gly		
130	135	140
Arg Pro Tyr Pro Pro Tyr Ser Leu Ala Asp Phe Ser Trp Asn Asn Ile		
145	150	155
Thr Asp Ser Leu Asp Pro Ala Thr Leu Ser Ala Thr Phe Gln Gly His		
165	170	175
Pro Met Asn Asp Pro Thr Arg Thr Phe Ala Asn Gly Ser Leu Ala Phe		
180	185	190
Arg Val Gln Ala Phe Ser Arg Ser Ser Arg Pro Ala Gln Pro Pro Arg		
195	200	205
Leu Leu His Thr Ala Asp Thr Cys Gln Leu Glu Val Ala Leu Ile Gly		
210	215	220
Ala Ser Pro Arg Gly Asn Arg Ser Leu Phe Gly Leu Glu Val Ala Thr		
225	230	235
Leu Gly Gln Gly Pro Asp Cys Pro Ser Met Gln Glu Gln His Ser Ile		
245	250	255
Asp Asp Glu Tyr Ala Pro Ala Val Phe Gln Leu Asp Gln Leu Leu Trp		
260	265	270
Gly Ser Leu Pro Ser Gly Phe Ala Gln Trp Arg Pro Val Ala Tyr Ser		
275	280	285

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Gln Lys Pro Gly Gly Arg Glu Ser Ala Leu Pro Cys Gln Ala Ser Pro

290 295 300

Leu His Pro Ala Leu Ala Tyr Ser Leu Pro Gln Ser Pro Ile Val Arg

305 310 315 320

Ala Phe Phe Gly Ser Gln Asn Asn Phe Cys Ala Phe Asn Leu Thr Phe

325 330 335

Gly Ala Ser Thr Gly Pro Gly Tyr Trp Asp Gln His Tyr Leu Ser Trp

340 345 350

Ser Met Leu Leu Gly Val Gly Phe Pro Pro Val Asp Gly Leu Ser Pro

355 360 365

Leu Val Leu Gly Ile Met Ala Val Ala Leu Gly Ala Pro Gly Leu Met

370 375 380

Leu Leu Gly Gly Gly Leu Val Leu Leu Leu His His Lys Lys Tyr Ser

385 390 395 400

Glu Tyr Gln Ser Ile Asn

405

<210> 10

<211> 192

<212> PRT

<213> Homo sapiens

<400> 10

Met Thr Ala Val Gly Val Gln Ala Gln Arg Pro Leu Gly Gln Arg Gln

1 5 10 15

Pro Arg Arg Ser Phe Phe Glu Ser Phe Ile Arg Thr Leu Ile Ile Thr

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20 25 30
Cys Val Ala Leu Ala Val Val Leu Ser Ser Val Ser Ile Cys Asp Gly
35 40 45
His Trp Leu Leu Ala Glu Asp Arg Leu Phe Gly Leu Trp His Phe Cys
50 55 60
Thr Thr Thr Asn Gln Ser Val Pro Ile Cys Phe Arg Asp Leu Gly Gln
65 70 75 80
Ala His Val Pro Gly Leu Ala Val Gly Met Gly Leu Val Arg Ser Val
85 90 95
Gly Ala Leu Ala Val Val Ala Ala Ile Phe Gly Leu Glu Phe Leu Met
100 105 110
Val Ser Gln Leu Cys Glu Asp Lys His Ser Gln Cys Lys Trp Val Met
115 120 125
Gly Ser Ile Leu Leu Leu Val Ser Phe Val Leu Ser Ser Gly Gly Leu
130 135 140
Leu Gly Phe Val Ile Leu Leu Arg Asn Gln Val Thr Leu Ile Gly Phe
145 150 155 160
Thr Leu Met Phe Trp Cys Glu Phe Thr Ala Ser Phe Leu Leu Phe Leu
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<210> 11

<211> 801

<212> DNA

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<213> Homo sapiens

<400> 11

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<211> 1257

<212> DNA

<213> Homo sapiens

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gtgacgggtg aggagcccgg ccggggcgcc ccgtcacgt ttcgcatcga ccggggcgcc    180
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<210> 13

<211> 1245

<212> DNA

<213> Homo sapiens

<400> 13

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<211> 1140

<212> DNA

<213> Homo sapiens

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<400> 14

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<210> 15

<211> 1755

<212> DNA

<213> Homo sapiens

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<400> 15

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 cacaaccag ctgggggcga ctatgcctct gtgaggacag cattgctggc agctagggct 1680
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<210> 16

<211> 993

<212> DNA

<213> Homo sapiens

<400> 16

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<210> 17

<211> 1035

<212> DNA

<213> Homo sapiens

<400> 17

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<211> 267

<212> DNA

<213> Homo sapiens

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accgggcac agagcctcac agaccccacc agctactacc tctccagcgt ctggagcttc 180
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<210> 19

<211> 1218

<212> DNA

<213> Homo sapiens

<400> 19

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gcagtgggca ccaattccac actgcactat gtgtggagca gcctggggcc tctggcagtg 240
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 ttgggccagg gccctgactg cccctcaatg caggagcagc actccatcga cgatgaatat 780
 gcaccggccg tcttcagtt ggaccagcta ctgtggggct cctcccatc aggctttgca 840
 cagtggcgac cagtggctta ctcccagaag ccggggggcc gagaatcagc cctgccctgc 900
 caagcttccc ctcttcatcc tgccttagca tactctcttc ccagtcacc cattgtccga 960
 gccttctttg ggtcccagaa taacttctgt gccttcaatc tgacgttcgg ggcttccaca 1020
 ggccctggct attgggacca aactacctc agcttgctga tgctcctggg tgtgggtctc 1080
 cctccagtgg acggcttgtc cccactagtc ctgggcatca tggcagtggc cctgggtgcc 1140
 ccagggtca tgctgctagg gggcggttg gttctgtgc tgcaccaca gaagtactca 1200
 gagtaccagt ccataaat 1218

<210> 20

<211> 576

<212> DNA

<213> Homo sapiens

<400> 20

atgactgccg tcggcgtgca ggcccagagg cctttgggcc aaaggcagcc ccgccgtcc 60
 ttctttgaat cttcatccg gacctcatc atcacgtgtg tggccctggc tgtgtcctg 120
 tcctcggtct ccatttgtga tgggcactgg ctctggctg aggaccgct ctcgggctc 180

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tggcacttct gcaccaccac caaccagagt gtgccgatct gcttcagaga cctgggccag 240
 gcccatgtgc ccgggctggc cgtgggcatg ggccctggtae gcagcgtggg cgccttggcc 300
 gtggtggccg ccatttttgg cctggagttc ctcattgtgt ccagttgtg cgaggacaaa 360
 cactcacagt gcaagtgggt catgggttcc atcctcctcc tgggtgtttt cgtcctctcc 420
 tccggcgggc tcctgggttt tgtgacctc ctcaggaacc aagtcacact catcggttc 480
 accctaattg tttggtgga attcactgcc tcctcctcc tctcctgaa cgccatcagc 540
 ggccctcaca tcaacagcat caccatccc tgggaa 576

<210> 21

<211> 2042

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)... (894)

<400> 21

tccggtgcct gcagagctcg gagcggcgga ggcagagacc gaggtgcac cggcagaggc 60
 tgcggggcgg acgcgcgggc cggcgcagcc atg gtg aag att agc ttc cag 111

Met Val Lys Ile Ser Phe Gln

1

5

ccc gcc gtg gct ggc atc aag ggc gac aag gct gac aag gcg tcg gcg 159
 Pro Ala Val Ala Gly Ile Lys Gly Asp Lys Ala Asp Lys Ala Ser Ala

10

15

20

tcg gcc cct gcg ccg gcc tcg gcc acc gag atc ctg ctg acg ccg gct. 207
 Ser Ala Pro Ala Pro Ala Ser Ala Thr Glu Ile Leu Leu Thr Pro Ala

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25	30	35	
agg gag gag cag ccc cca caa cat cga tcc aag agg ggg agc tca gtg			255
Arg Glu Glu Gln Pro Pro Gln His Arg Ser Lys Arg Gly Ser Ser Val			
40	45	50	55
ggc ggc gtg tgc tac ctg tcg atg ggc atg gtc gtg ctg ctc atg ggc			303
Gly Gly Val Cys Tyr Leu Ser Met Gly Met Val Val Leu Leu Met Gly			
60	65	70	
ctc gtg ttc gcc tct gtc tac atc tac aga tac ttc ttt ctt gca cag			351
Leu Val Phe Ala Ser Val Tyr Ile Tyr Arg Tyr Phe Phe Leu Ala Gln			
75	80	85	
ctg gcc cga gat aac ttc ttc cgc tgt ggt gtg ctg tat gag gac tcc			399
Leu Ala Arg Asp Asn Phe Phe Arg Cys Gly Val Leu Tyr Glu Asp Ser			
90	95	100	
ctg tcc tcc cag gtc cgg act cag atg gag ctg gaa gag gat gtg aaa			447
Leu Ser Ser Gln Val Arg Thr Gln Met Glu Leu Glu Glu Asp Val Lys			
105	110	115	
atc tac ctc gac gag aac tac gag cgc atc aac gtg cct gtg ccc cag			495
Ile Tyr Leu Asp Glu Asn Tyr Glu Arg Ile Asn Val Pro Val Pro Gln			
120	125	130	135
ttt ggc ggc ggt gac cct gca gac atc atc cat gac ttc cag cgg ggt			543
Phe Gly Gly Gly Asp Pro Ala Asp Ile Ile His Asp Phe Gln Arg Gly			
140	145	150	
ctg act gcg tac cat gat atc tcc ctg gac aag tgc tat gtc atc gaa			591
Leu Thr Ala Tyr His Asp Ile Ser Leu Asp Lys Cys Tyr Val Ile Glu			
155	160	165	

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ctc aac acc acc att gtg ctg ccc cct cgc aac ttc tgg gag ctc ctc 639

Leu Asn Thr Thr Ile Val Leu Pro Pro Arg Asn Phe Trp Glu Leu Leu

170 175 180

atg aac gtg aag agg ggg acc tac ctg ccg cag acg tac atc atc cag 687

Met Asn Val Lys Arg Gly Thr Tyr Leu Pro Gln Thr Tyr Ile Ile Gln

185 190 195

gag gag atg gtg gtc acg gag cat gtc agt gac aag gag gcc ctg ggg 735

Glu Glu Met Val Val Thr Glu His Val Ser Asp Lys Glu Ala Leu Gly

200 205 210 215

tcc ttc atc tac cac ctg tgc aac ggg aaa gac acc tac cgg ctc cgg 783

Ser Phe Ile Tyr His Leu Cys Asn Gly Lys Asp Thr Tyr Arg Leu Arg

220 225 230

cgc cgg gca acg cgg agg cgg atc aac aag cgt ggg gcc aag aac tgc 831

Arg Arg Ala Thr Arg Arg Arg Ile Asn Lys Arg Gly Ala Lys Asn Cys

235 240 245

aat gcc atc cgc cac ttc gag aac acc ttc gtg gtg gag acg ctc atc 879

Asn Ala Ile Arg His Phe Glu Asn Thr Phe Val Val Glu Thr Leu Ile

250 255 260

tgc ggg gtg gtg tgaggccctc ctccccaga accccctgcc gtgttctc 930

Cys Gly Val Val

265

ttttcttctt tccggtgct ctctggccct cctccttccc cctgcttagc ttgtactttg 990

gacgcgtttc tatagagggtg acatgtctct ccttctctt ccaacctgc ccacctcct 1050

gtaccagagc tgtgatctct cgggtgggggg cccatctctg ctgacctggg tgtggcggag 1110

ggagaggcga tgctgcaaag tgttttctgt gtcccactgt cttgaagctg ggcctgcca 1170

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agcctgggccc cacagctgca ccggcagccc aaggggaagg accggttggg ggagccgggc 1230
atgtgaggcc ctgggcaagg ggatggggct gtggggcgcg ggcgcatgg gcttcagaag 1290
tatctgcaca attagaaaag tcctcagaag ctttttcttg gagggtacac tttcttcaact 1350
gtccctattc ctagacctgg ggcttgagct gaggatggga cgatgtgccc agggagggac 1410
ccaccagagc acaagagaag gtggctacct ggggggtgcc cagggactct gtcagtgcct 1470
tcagcccacc agcaggagct tggagtttgg ggagtgggga tgagtccgtc aagcacaact 1530
gttctctgag tggaacaaaa gaagcaagga gctaggaccc ccagtcctgc cccccaggag 1590
cacaagcagg gtccctcag tcaaggcagt gggatgggcg gctgaggaac ggggcaggca 1650
aggtcactgc tcagtcacgt ccacggggga cgagccgtgg gttctgctga gtaggtggag 1710
ctcattgctt tctccaagct tggaactggt ttgaaagata acacagaggg aaaggagag 1770
ccacctggta ctgtccacc ctgctctc tcgttctgaaa ttccatcccc ctcaagcttag 1830
gggaatgcac ctttttcct ttccttctca cttttgcatg tttttactga tcattcgata 1890
tgctaaccgt tctcagccct gaccccttga gaggagggct gtaacgcctt cagtcagtct 1950
ctggggatga aactcttaaa tgctttgtat attttctcaa ttagatctct tttcagaagt 2010
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<210> 22

<211> 1433

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (5)... (1264)

<400> 22

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Met Ser Cys Ala Gly Arg Ala Gly Pro Ala Arg Leu Ala Ala

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1	5	10	
ctc gcc ctg ctg acc tgc agc ctg tgg ccg gca cgg gca gac aac gcg			94
Leu Ala Leu Leu Thr Cys Ser Leu Trp Pro Ala Arg Ala Asp Asn Ala			
15	20	25	30
agc cag gag tac tac acg gcg ctc atc aac gtg acg gtg cag gag ccc			142
Ser Gln Glu Tyr Tyr Thr Ala Leu Ile Asn Val Thr Val Gln Glu Pro			
35	40	45	
ggc cgc ggc gcc ccg ctc acg ttt cgc atc gac cgc ggg cgc tac ggg			190
Gly Arg Gly Ala Pro Leu Thr Phe Arg Ile Asp Arg Gly Arg Tyr Gly			
50	55	60	
ctt gac tcc ccc aag gcc gag gtc cgc ggc cag gtg ctg gcg ccg ctg			238
Leu Asp Ser Pro Lys Ala Glu Val Arg Gly Gln Val Leu Ala Pro Leu			
65	70	75	
ccc ctc cac gga gtt gct gat cat ctg ggc tgt gat cca caa acc cgg			286
Pro Leu His Gly Val Ala Asp His Leu Gly Cys Asp Pro Gln Thr Arg			
80	85	90	
ttc ttt gtc cct cct aat atc aaa cag tgg att gcc ttg ctg cag agg			334
Phe Phe Val Pro Pro Asn Ile Lys Gln Trp Ile Ala Leu Leu Gln Arg			
95	100	105	110
gga aac tgc acg ttt aaa gag aaa ata tca cgg gcc gct ttc cac aat			382
Gly Asn Cys Thr Phe Lys Glu Lys Ile Ser Arg Ala Ala Phe His Asn			
115	120	125	
gca gtt gct gta gtc atc tac aat aat aaa tcc aaa gag gag cca gtt			430
Ala Val Ala Val Val Ile Tyr Asn Asn Lys Ser Lys Glu Glu Pro Val			
130	135	140	

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acc atg act cat cca ggc act gga gat att att gct gtc atg ata aca 478
Thr Met Thr His Pro Gly Thr Gly Asp Ile Ile Ala Val Met Ile Thr
145 150 155

gaa ttg agg ggt aag gat att ttg agt tat ctg gag aaa aac atc tct 526
Glu Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser
160 165 170

gta caa atg aca ata gct gtt gga act cga atg cca ccg aag aac ttc 574
Val Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe
175 180 185 190

agc cgt ggc tct cta gtc ttc gtg tca ata tcc ttt att gtt ttg atg 622
Ser Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met
195 200 205

att att tct tca gca tgg ctc ata ttc tac ttc att cag aag atc agg 670
Ile Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg
210 215 220

tac aca aat gca cgc gac agg aac cag cgt cgt ctc gga gat gca gcc 718
Tyr Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala
225 230 235

aag aaa gcc atc agt aaa ttg aca acc agg aca gta aag aag ggt gac 766
Lys Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp
240 245 250

aag gaa act gac cca gac ttt gat cat tgt gca gtc tgc ata gag agc 814
Lys Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser
255 260 265 270

tat aag cag aat gat gtc gtc cga att ctc ccc tgc aag cat gtt ttc 862

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Tyr Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe
 275 280 285
 cac aaa tcc tgc gtg gat ccc tgg ctt agt gaa cat tgt acc tgt cct 910
 His Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro
 290 295 300
 atg tgc aaa ctt aat ata ttg aag gcc ctg gga att gtg ccg aat ttg 958
 Met Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu
 305 310 315
 cca tgt act gat aac gta gca ttc gat atg gaa agg ctc acc aga acc 1006
 Pro Cys Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr
 320 325 330
 caa gct gtt aac cga aga tca gcc ctc ggc gac ctc gcc ggc gac aac 1054
 Gln Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn
 335 340 345 350
 tcc ctt ggc ctt gag cca ctt cga act tcg ggg atc tca cct ctt cct 1102
 Ser Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro
 355 360 365
 cag gat ggg gag ctc act ccg aga aca gga gaa atc aac att gca gta 1150
 Gln Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val
 370 375 380
 aca aaa gaa tgg ttt att att gcc agt ttt ggc ctc ctc agt gcc ctc 1198
 Thr Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu
 385 390 395
 aca ctc tgc tac atg atc atc aga gcc aca gct agc ttg aat gct aat 1246
 Thr Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn

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400 405 410
gag gta gaa tgg ttt tgaagaagaa aaaacctgct ttctgactga ttttgcctt 1300
Glu Val Glu Trp Phe
415
gaaggaaaaa agaacctatt tttgtgcatc atttaccat catgccacac aagcatttat 1360
ttttagtaca ttttattttt tcataaaatt gctaatacca aagctttgta ttaaaagaaa 1420
taaataataa aat 1433

<210> 23

<211> 1917

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (210)... (1457)

<400> 23

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cagccgagcg ccggtgtgag ccagcgctgc tgccagtgtg agccagcgt gctgccagtg 120
tgagcggcgg tgtgagcgcg gtgggtgcgg aggggcgtgt gtgccggcgc gcgcgccgtg 180
gggtgcaaac ccgagcgtc tacgtgcc atg agg ggc gcg aac gcc tgg gcg 233

Met Arg Gly Ala Asn Ala Trp Ala

1 5

cca ctc tgc ctg ctg ctg gct gcc gcc acc cag ctc tcg cgg cag cag 281

Pro Leu Cys Leu Leu Leu Ala Ala Ala Thr Gln Leu Ser Arg Gln Gln

10 15 20

• • • • •

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Tyr Cys Gly Gly Leu Leu Asp Arg Pro Ser Gly Ser Phe Lys Thr Pro
155 160 165
aac tgg cca gac cgg gat tac cct gca gga gtc act tgt gtg tgg cac 761
Asn Trp Pro Asp Arg Asp Tyr Pro Ala Gly Val Thr Cys Val Trp His
170 175 180
att gta gcc cca aag aat cag ctt ata gaa tta aag ttt gag aag ttt 809
Ile Val Ala Pro Lys Asn Gln Leu Ile Glu Leu Lys Phe Glu Lys Phe
185 190 195 200
gat gtg gag cga gat aac tac tgc cga tat gat tat gtg gct gtg ttt 857
Asp Val Glu Arg Asp Asn Tyr Cys Arg Tyr Asp Tyr Val Ala Val Phe
205 210 215
aat ggc ggg gaa gtc aac gat gct aga aga att gga aag tat tgt ggt 905
Asn Gly Gly Glu Val Asn Asp Ala Arg Arg Ile Gly Lys Tyr Cys Gly
220 225 230
gat agt cca cct gcg cca att gtg tct gag aga aat gaa ctt ctt att 953
Asp Ser Pro Pro Ala Pro Ile Val Ser Glu Arg Asn Glu Leu Leu Ile
235 240 245
cag ttt tta tca gac tta agt tta act gca gat ggg ttt att ggt cac 1001
Gln Phe Leu Ser Asp Leu Ser Leu Thr Ala Asp Gly Phe Ile Gly His
250 255 260
tac ata ttc agg cca aaa aaa ctg cct aca act aca gaa cag cct gtc 1049
Tyr Ile Phe Arg Pro Lys Lys Leu Pro Thr Thr Thr Glu Gln Pro Val
265 270 275 280
acc acc aca ttc cct gta acc acg ggt tta aaa acc acc gtg gcc ttg 1097
Thr Thr Thr Phe Pro Val Thr Thr Gly Leu Lys Thr Thr Val Ala Leu

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285	290	295	
tgt caa caa aag tgt aga cgg acg ggg act ctg gag ggc aat tat tgt			1145
Cys Gln Gln Lys Cys Arg Arg Thr Gly Thr Leu Glu Gly Asn Tyr Cys			
300	305	310	
tca agt gac ttt gta tta gcc ggc act gtt atc aca acc atc act cgc			1193
Ser Ser Asp Phe Val Leu Ala Gly Thr Val Ile Thr Thr Ile Thr Arg			
315	320	325	
gat ggg agt ttg cac gcc aca gtc tcg atc atc aac atc tac aaa gag			1241
Asp Gly Ser Leu His Ala Thr Val Ser Ile Ile Asn Ile Tyr Lys Glu			
330	335	340	
gga aat ttg gcg att cag cag gcg ggc aag aac atg agt gcc agg ctg			1289
Gly Asn Leu Ala Ile Gln Gln Ala Gly Lys Asn Met Ser Ala Arg Leu			
345	350	355	360
act gtc gtc tgc aag cag tgc cct ctc ctc aga aga ggt cta aat tac			1337
Thr Val Val Cys Lys Gln Cys Pro Leu Leu Arg Arg Gly Leu Asn Tyr			
365	370	375	
att att atg ggc caa gta ggt gaa gat ggg cga ggc aaa atc atg cca			1385
Ile Ile Met Gly Gln Val Gly Glu Asp Gly Arg Gly Lys Ile Met Pro			
380	385	390	
aac agc ttt atc atg atg ttc aag acc aag aat cag aag ctc ctg gat			1433
Asn Ser Phe Ile Met Met Phe Lys Thr Lys Asn Gln Lys Leu Leu Asp			
395	400	405	
gcc tta aaa aat aag caa tgt taacagtga ctgtgtccat ttaagc			1480
Ala Leu Lys Asn Lys Gln Cys			
410	415		

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tgtattctgc cattgccttt gaaagatcta tgttctctca gtagaaaaaa aaatacttat 1540
 aaaattacat attctgaaag aggattccga aagatgggac tggttgactc ttcacatgat 1600
 ggaggtatga ggcctccgag atagctgagg gaagttcttt gcctgctgtc agaggagcag 1660
 ctatctgatt ggaaacctgc cgacttagtg cggatgatagg aagctaaaag tgtcaagcgt 1720
 tgacagcttg gaagcgttta tttatacatc tctgtaaaag gatatttttag aattgagttg 1780
 tgtgaagatg tcaaaaaaag attttagaag tgcaatattt atagtgttat ttgtttcacc 1840
 ttcaagcctt tgcctgagg tgttacaatc ttgtcttgcg ttttctaaat caatgcttaa 1900
 taaaatattt ttaaagg 1917

<210> 24

<211> 2258

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225)... (1367)

<400> 24

tttttcccg ctagggctcg gctcagctcg actgggctcg gcgggcggcg gcggcggcgc 60
 ccgcggctgg cggaggaggg agggcgaggg cgggcgcggg ccggcgggcg gcgggaagag 120
 ggaggagagg cgcgggggag caggcctcgg ggccctcggag caaccacccg agcagacgga 180
 gtacacggag cagcggcccc ggccccgcca acgctgccgc cggg atg etc cag 233

Met Leu Gln

1

acc ttg tat gat tac ttc tgg tgg gaa cgt ctg tgg ctg cct gtg aac 281

Thr Leu Tyr Asp Tyr Phe Trp Trp Glu Arg Leu Trp Leu Pro Val Asn

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5	10	15	
ttg acc tgg gcc gat cta gaa gac cga gat gga cgt gtc tac gcc aaa			329
Leu Thr Trp Ala Asp Leu Glu Asp Arg Asp Gly Arg Val Tyr Ala Lys			
20	25	30	35
gcc tca gat ctc tat atc acg ctg ccc ctg gcc ttg ctc ttc ctc atc			377
Ala Ser Asp Leu Tyr Ile Thr Leu Pro Leu Ala Leu Leu Phe Leu Ile			
40	45	50	
gtt cga tac ttc ttt gag ctg tac gtg gct aca cca ctg gct gcc ctc			425
Val Arg Tyr Phe Phe Glu Leu Tyr Val Ala Thr Pro Leu Ala Ala Leu			
55	60	65	
ttg aac ata aag gag aaa act cgg ctg cgg gca cct ccc aac gcc acc			473
Leu Asn Ile Lys Glu Lys Thr Arg Leu Arg Ala Pro Pro Asn Ala Thr			
70	75	80	
ttg gaa cat ttc tac ctg acc agt ggc aag cag ccc aag cag gtg gaa			521
Leu Glu His Phe Tyr Leu Thr Ser Gly Lys Gln Pro Lys Gln Val Glu			
85	90	95	
gta gag ctt ttg tcc cgg cag agc ggg ctc tct ggc cgc cag gta gag			569
Val Glu Leu Leu Ser Arg Gln Ser Gly Leu Ser Gly Arg Gln Val Glu			
100	105	110	115
cgt tgg ttc cgt cgc cgc cgc aac cag gac cgg ccc agt ctc ctc aag			617
Arg Trp Phe Arg Arg Arg Arg Asn Gln Asp Arg Pro Ser Leu Leu Lys			
120	125	130	
aag ttc cga gaa gcc agc tgg aga ttc aca ttt tac ctg att gcc ttc			665
Lys Phe Arg Glu Ala Ser Trp Arg Phe Thr Phe Tyr Leu Ile Ala Phe			
135	140	145	

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att gcc ggc atg gcc gtc att gtg gat aaa ccc tgg ttc tat gac atg 713
 Ile Ala Gly Met Ala Val Ile Val Asp Lys Pro Trp Phe Tyr Asp Met
 150 155 160
 aag aaa gtt tgg gag gga tat ccc ata cag agc act atc cct tcc cag 761
 Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile Pro Ser Gln
 165 170 175
 tat tgg tac tac atg att gaa ctt tcc ttc tac tgg tcc ctg ctc ttc 809
 Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser Leu Leu Phe
 180 185 190 195
 agc att gcc tct gat gtc aag cga aag gat ttc aag gaa cag atc atc 857
 Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu Gln Ile Ile
 200 205 210
 cac cat gtg gcc acc atc att ctc atc agc ttt tcc tgg ttt gcc aat 905
 His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp Phe Ala Asn
 215 220 225
 tac atc cga gct ggg act cta atc atg gct ctg cat gac tct tcc gat 953
 Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp Ser Ser Asp
 230 235 240
 tac ctg ctg gag tca gcc aag atg ttt aac tac gcg gga tgg aag aac 1001
 Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly Trp Lys Asn
 245 250 255
 acc tgc aac aac atc ttc atc gtc ttc gcc att gtt ttt atc atc acc 1049
 Thr Cys Asn Asn Ile Phe Ile Val Phe Ala Ile Val Phe Ile Ile Thr
 260 265 270 275
 cga ctg gtc atc ctg ccc ttc tgg atc ctg cat tgc acc ctg gtg tac 1097

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Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys Thr Leu Val Tyr
 280 285 290
 cca ctg gag ctc tat cct gcc ttc ttt ggc tat tac ttc ttc aat tcc 1145
 Pro Leu Glu Leu Tyr Pro Ala Phe Phe Gly Tyr Tyr Phe Phe Asn Ser
 295 300 305
 atg atg gga gtt cta cag ctg ctg cat atc ttc tgg gcc tac ctc att 1193
 Met Met Gly Val Leu Gln Leu Leu His Ile Phe Trp Ala Tyr Leu Ile
 310 315 320
 ttg cgc atg gcc cac aag ttc ata act gga aag ctg gta gaa gat gaa 1241
 Leu Arg Met Ala His Lys Phe Ile Thr Gly Lys Leu Val Glu Asp Glu
 325 330 335
 cgc agt gac cgg gaa gaa aca gag agc tca gag ggg gag gag gct gca 1289
 Arg Ser Asp Arg Glu Glu Thr Glu Ser Ser Glu Gly Glu Glu Ala Ala
 340 345 350 355
 gct ggg gga gga gca aag agc cgg ccc cta gcc aat ggc cac ccc atc 1337
 Ala Gly Gly Gly Ala Lys Ser Arg Pro Leu Ala Asn Gly His Pro Ile
 360 365 370
 ctc aat aac aac cat cgt aag aat gac tgaaccatta ttccagctgc ctccca 1390
 Leu Asn Asn Asn His Arg Lys Asn Asp
 375 380
 gattaatgca taaagccaag gaactaccct gctccctgcg ctatagggtc actttaagct 1450
 ctggggaaaa aggagaaagt gagaggagag ttctctgcat cctccctcct tgcttgac 1510
 ccagttgcct ttaaaccaaa ttctaaccag cctatcccca ggtaggggga cgttggttat 1570
 attctgttag agggggacgg tcgtattttc ctccctaccc gccaaagtcac cctttctact 1630
 gcttttgagg cctccctca gctctctgtg ggtaggggtt acaattcaca ttcttatto 1690

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tgagaatttg gccccagctg tttgcctttg actccctgac ctccagagcc agggttgtgc 1750
 cttattgtcc catctgtggg cctcattctg ccaaagctgg accaaggcta acctttctaa 1810
 gctccctaac ttgggccaga aaccaaagct gagcttttaa ctttctccct ctatgacaca 1870
 aatgaattga gggtaggagg aggggtgcaca taacccttac cctacctctg ccaaaaagtg 1930
 ggggctgtac tggggactgc tcggatgac tttcttagtg ctacttcttt cagctgtccc 1990
 tgtagcgaca ggtctaagat ctgactgcct cctttctctg gcctcttccc ccttccctct 2050
 tctcttcagc taggctagct ggtttggagt agaattggcaa ctaattctaa tttttattta 2110
 ttaaataattt ggggttttgg ttttaaagcc agaattacgg ctagcaccta gcatttcagc 2170
 agagggacca ttttagacca aaatgtactg ttaatgggtt tttttttaaa attaaaagat 2230
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<210> 25

<211> 1973

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (130)... (1887)

<400> 25

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 agcgtcgcc atg gtc tgc agg gag cag tta tca aag aat cag gtc aag 168

Met Val Cys Arg Glu Gln Leu Ser Lys Asn Gln Val Lys

1

5

10

tgg gtg ttt gcc ggc att acc tgt gtg tct gtg gtg gtc att gcc gca 216

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Trp Val Phe Ala Gly Ile Thr Cys Val Ser Val Val Val Ile Ala Ala
 15 20 25
 ata gtc ctt gcc atc acc ctg cgg cgg cca ggc tgt gag ctg gag gcc 264
 Ile Val Leu Ala Ile Thr Leu Arg Arg Pro Gly Cys Glu Leu Glu Ala
 30 35 40 45
 tgc agc cct gat gcc gac atg ctg gac tac ctg ctg agc ctg ggc cag 312
 Cys Ser Pro Asp Ala Asp Met Leu Asp Tyr Leu Leu Ser Leu Gly Gln
 50 55 60
 atc agc cgg cga gat gcc ttg gag gtc acc tgg tac cac gca gcc aac 360
 Ile Ser Arg Arg Asp Ala Leu Glu Val Thr Trp Tyr His Ala Ala Asn
 65 70 75
 agc aag aaa gcc atg aca gct gcc ctg aac agc aac atc aca gtc ctg 408
 Ser Lys Lys Ala Met Thr Ala Ala Leu Asn Ser Asn Ile Thr Val Leu
 80 85 90
 gag gct gac gtc aat gta gaa ggg ctc ggc aca gcc aat gag aca gga 456
 Glu Ala Asp Val Asn Val Glu Gly Leu Gly Thr Ala Asn Glu Thr Gly
 95 100 105
 gtt ccc atc atg gca cac ccc ccc act atc tac agt gac aac aca ctg 504
 Val Pro Ile Met Ala His Pro Pro Thr Ile Tyr Ser Asp Asn Thr Leu
 110 115 120 125
 gag cag tgg ctg gac gct gtg ctg ggc tct tcc caa aag ggc atc aaa 552
 Glu Gln Trp Leu Asp Ala Val Leu Gly Ser Ser Gln Lys Gly Ile Lys
 130 135 140
 ctg gac ttc aag aac atc aag gca gtg ggc ccc tcc ctg gac ctc ctg 600
 Leu Asp Phe Lys Asn Ile Lys Ala Val Gly Pro Ser Leu Asp Leu Leu

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145	150	155	
cgg cag ctg aca gag gaa ggc aaa gtc cgg cgg ccc ata tgg atc aac			648
Arg Gln Leu Thr Glu Glu Gly Lys Val Arg Arg Pro Ile Trp Ile Asn			
160	165	170	
gct gac atc tta aag ggc ccc aac atg ctc atc tca act gag gtc aat			696
Ala Asp Ile Leu Lys Gly Pro Asn Met Leu Ile Ser Thr Glu Val Asn			
175	180	185	
gcc aca cag ttc ctg gcc ctg gtc cag gag aag tat ccc aag gct acc			744
Ala Thr Gln Phe Leu Ala Leu Val Gln Glu Lys Tyr Pro Lys Ala Thr			
190	195	200	205
cta tct cca ggc tgg acc acc ttc tac atg tcc acg tcc cca aac agg			792
Leu Ser Pro Gly Trp Thr Thr Phe Tyr Met Ser Thr Ser Pro Asn Arg			
210	215	220	
acg tac acc caa gcc atg gtg gag aag atg cac gag ctg gtg gga gga			840
Thr Tyr Thr Gln Ala Met Val Glu Lys Met His Glu Leu Val Gly Gly			
225	230	235	
gtg ccc cag agg gtc acc ttc cct gta cgg tct tcc atg gtg cgg gct			888
Val Pro Gln Arg Val Thr Phe Pro Val Arg Ser Ser Met Val Arg Ala			
240	245	250	
gcc tgg ccc cac ttc agc tgg ctg ctg agc caa tct gag agg tac agc			936
Ala Trp Pro His Phe Ser Trp Leu Leu Ser Gln Ser Glu Arg Tyr Ser			
255	260	265	
ctg acg ctg tgg cag gct gcc tcg gac ccc atg tcg gtg gaa gat ctg			984
Leu Thr Leu Trp Gln Ala Ala Ser Asp Pro Met Ser Val Glu Asp Leu			
270	275	280	285

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ctc tac gtc cgg gat aac act gct gtc cac caa gtc tac tat gac atc 1032
 Leu Tyr Val Arg Asp Asn Thr Ala Val His Gln Val Tyr Tyr Asp Ile
 290 295 300
 ttt gag cct ctc ctg tca cag ttc aag cag ctg gcc ttg aat gcc aca 1080
 Phe Glu Pro Leu Leu Ser Gln Phe Lys Gln Leu Ala Leu Asn Ala Thr
 305 310 315
 cgg aaa cca atg tac tac aca gga ggc agc ctg atc cct ctt ctc cag 1128
 Arg Lys Pro Met Tyr Tyr Thr Gly Gly Ser Leu Ile Pro Leu Leu Gln
 320 325 330
 ctg cct ggg gat gac ggt ctg aat gtg gag tgg ctg gtt cct gac gtc 1176
 Leu Pro Gly Asp Asp Gly Leu Asn Val Glu Trp Leu Val Pro Asp Val
 335 340 345
 cag ggc agc ggt aaa aca gca aca atg acc ctc cca gac aca gaa ggc 1224
 Gln Gly Ser Gly Lys Thr Ala Thr Met Thr Leu Pro Asp Thr Glu Gly
 350 355 360 365
 atg atc ctg ctg aac act ggc ctc gag gga act gtg gct gaa aac ccc 1272
 Met Ile Leu Leu Asn Thr Gly Leu Glu Gly Thr Val Ala Glu Asn Pro
 370 375 380
 gtg ccc att gtt cat act cca agt ggc aac atc ctg acg ctg gag tcc 1320
 Val Pro Ile Val His Thr Pro Ser Gly Asn Ile Leu Thr Leu Glu Ser
 385 390 395
 tgc ctg cag cag ctg gcc aca cat ccc gga cac tgg ggc atc cat ttg 1368
 Cys Leu Gln Gln Leu Ala Thr His Pro Gly His Trp Gly Ile His Leu
 400 405 410
 caa ata gcg gag ccc gca gcc ctc cgg cca tcc ctg gcc ttg ctg gca 1416

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Gln Ile Ala Glu Pro Ala Ala Leu Arg Pro Ser Leu Ala Leu Leu Ala
415 420 425
cgc ctc tcc agc ctt ggc ctc ttg cat tgg cct gtg tgg gtt ggg gcc 1464
Arg Leu Ser Ser Leu Gly Leu Leu His Trp Pro Val Trp Val Gly Ala
430 435 440 445
aaa atc tcc cac ggg agt ttt tgc gtc ccc ggc cat gtg gct ggc aga 1512
Lys Ile Ser His Gly Ser Phe Ser Val Pro Gly His Val Ala Gly Arg
450 455 460
gag ctg ctt aca gct gtg gct gag gtc ttc ccc cac gtg act gtg gca 1560
Glu Leu Leu Thr Ala Val Ala Glu Val Phe Pro His Val Thr Val Ala
465 470 475
cca ggc tgg cct gag gag gtg ctg ggc agt ggc tac agg gaa cag ctg 1608
Pro Gly Trp Pro Glu Glu Val Leu Gly Ser Gly Tyr Arg Glu Gln Leu
480 485 490
ctc aca gat atg cta gag ttg tgc cag ggg ctc tgg caa cct gtg tcc 1656
Leu Thr Asp Met Leu Glu Leu Cys Gln Gly Leu Trp Gln Pro Val Ser
495 500 505
ttc cag atg cag gcc atg ctg ctg ggc cac agc aca gct gga gcc ata 1704
Phe Gln Met Gln Ala Met Leu Leu Gly His Ser Thr Ala Gly Ala Ile
510 515 520 525
ggc agg ctg ctg gca tcc tcc ccc cgg gcc acc gtc aca gtg gag cac 1752
Gly Arg Leu Leu Ala Ser Ser Pro Arg Ala Thr Val Thr Val Glu His
530 535 540
aac cca gct ggg ggc gac tat gcc tct gtg agg aca gca ttg ctg gca 1800
Asn Pro Ala Gly Gly Asp Tyr Ala Ser Val Arg Thr Ala Leu Leu Ala

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545 550 555
 gct agg gct gtg gac agg acc cga gtc tac tac agg cta ccc cag ggc 1848
 Ala Arg Ala Val Asp Arg Thr Arg Val Tyr Tyr Arg Leu Pro Gln Gly

560 565 570
 tac cac aag gac ttg ctg gct cat gtt ggt aga aac tgagcaccca ggggtg 1900
 Tyr His Lys Asp Leu Leu Ala His Val Gly Arg Asn

575 580 585
 gtgggccagc ggacctcagg gcggaggctt cccacgggga ggcaggaaga aataaaggtc 1960
 ttggttttc tcc 1973

<210> 26

<211> 1606

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (135)... (1130)

<400> 26

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 cctcgtttct cgttctactg cccagaggagc ccggcgggtc cgggactccc gtccgtgccg 120
 gtgcgggcgc cggc atg tgg ctg tgg gag gac cag ggc ggc ctc ctg ggc 170

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly

1 5 10
 cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg cgg agc ccg 218
 Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro

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15	20	25	
gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta ctg cgc gtc			266
Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val			
30	35	40	
ttc agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag gtg ctc aag			314
Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys			
45	50	55	60
ccc cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc agc cac gac			362
Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp			
65	70	75	
gcg ccc gag aac acg ctg gcg gcc att cgg cag gca gct aag aat gga			410
Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly			
80	85	90	
gca aca ggc gtg gag ttg gac att gag ttt act tct gac ggg att cct			458
Ala Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro			
95	100	105	
gtc tta atg cac gat aac aca gta gat agg acg act gat ggg act ggg			506
Val Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly			
110	115	120	
cga ttg tgt gat ttg aca ttt gaa caa att agg aag ctg aat cct gca			554
Arg Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala			
125	130	135	140
gca aac cac aga ctc agg aat gat ttc cct gat gaa aag atc cct acc			602
Ala Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr			
145	150	155	

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cta agg gaa gct gtt gca gag tgc cta aac cat aac ctc aca atc ttc 650
Leu Arg Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe
160 165 170
ttt gat gtc aaa ggc cat gca cac aag gct act gag gct cta aag aaa 698
Phe Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys
175 180 185
atg tat atg gaa ttt cct caa ctg tat aat aat agt gtg gtc tgt tct 746
Met Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser
190 195 200
ttc ttg cca gaa gtt atc tac aag atg aga caa aca gat cgg gat gta 794
Phe Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val
205 210 215 220
ata aca gca tta act cac aga cct tgg agc cta agc cat aca gga gat 842
Ile Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp
225 230 235
ggg aaa cca cgc tat gat act ttc tgg aaa cat ttt ata ttt gtt atg 890
Gly Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met
240 245 250
atg gac att ttg ctc gat tgg agc atg cat aat atc ttg tgg tac ctg 938
Met Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu
255 260 265
tgt gga att tca gct ttc ctc atg caa aag gat ttt gta tcc ccg gcc 986
Cys Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala
270 275 280
tac ttg aag aag tgg tca gct aaa gga atc cag gtt gtt ggt tgg act 1034

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Tyr Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr
 285 290 295 300
 gtt aat acc ttt gat gaa aag agt tac tac gaa tcc cat ctt ggt tcc 1082
 Val Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser
 305 310 315
 agc tat atc act gac agc atg gta gaa gac tgc gaa cct cac ttc 1127
 Ser Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
 320 325 330
 tag actttcacgg tgggacgaaa cgggttcaga aactgccagg ggccctcatc 1180
 aggatatca aaataccctt tgtgctagcc caggccctgg ggaatcaggt gactcacaca 1240
 aatgcaatag ttggtcactg catttttacc tgaaccaaag ctaaaccggg tgttgccacc 1300
 atgcaccatg gcatgccaga gttcaacact gttgctcttg aaaatctggg tctgaaaaaa 1360
 cgcacaagag cccctgccct gccctagctg aggcacacag ggagaccag tgaggataag 1420
 cacagattga attgtacaat ttgcagatgc agatgtaaat gcatgggaca tgcattgataa 1480
 ctcagagttg acattttaaa acttgccaca cttatttcaa atatttgtac tcagctatgt 1540
 taacatgtac ttagacatc aaactgtgg ccatactaataaaaattatta aaaggagcac 1600
 taaagg 1606

<210> 27

<211> 2380

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (247)... (1284)

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<400> 27

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 ttcttccttg cccgccggg gccctgaccg tggtttcttc cccggcctga tctgcgcage 120
 ccggcggggc cccagaagga gcaggcggcg cgggggcgcg ctgggcgggg gaggcgtggc 180
 cggagctgcg gcggcaagcg ggctgggact gctcggccgc ctctgcccgc gcgagcagct 240
 cagacc atg tcg cct gaa gaa tgg acg tat cta gtg gtt ctt ctt atc 288

Met Ser Pro Glu Glu Trp Thr Tyr Leu Val Val Leu Leu Ile

. . . 1 5 10
 tcc atc ccc atc ggc ttc ctc ttt aag aaa gcc ggt cct ggg ctg aag 336

Ser Ile Pro Ile Gly Phe Leu Phe Lys Lys Ala Gly Pro Gly Leu Lys

15 20 25 30
 aga tgg gga gca gcc gct gtg ggc ctg ggg ctc acc ctg ttc acc tgt 384
 Arg Trp Gly Ala Ala Ala Val Gly Leu Gly Leu Thr Leu Phe Thr Cys

35 40 45
 ggc ccc cac act ttg cat tct ctg gtc acc atc ctc ggg acc tgg gcc 432
 Gly Pro His Thr Leu His Ser Leu Val Thr Ile Leu Gly Thr Trp Ala

. . . 50 55 60
 ctc att cag gcc cag ccc tgc tcc tgc cac gcc ctg gct ctg gcc tgg 480
 Leu Ile Gln Ala Gln Pro Cys Ser Cys His Ala Leu Ala Leu Ala Trp

. . . 65 70 75
 act ttc tcc tat ctc ctg ttc ttc cga gcc ctc agc ctc ctg ggc ctg 528
 Thr Phe Ser Tyr Leu Leu Phe Phe Arg Ala Leu Ser Leu Leu Gly Leu

. . . 80 85 90
 ccc act ccc acg ccc ttc acc aat gcc gtc cag ctg ctg ctg acg ctg 576
 Pro Thr Pro Thr Pro Phe Thr Asn Ala Val Gln Leu Leu Leu Thr Leu

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95	100	105	110	
aag ctg gtg agc ctg gcc agt gaa gtc cag gac ctg cat ctg gcc cag				624
Lys Leu Val Ser Leu Ala Ser Glu Val Gln Asp Leu His Leu Ala Gln				
	115	120	125	
agg aag gaa atg gcc tca ggc ttc agc aag ggg ccc acc ctg ggg ctg				672
Arg Lys Glu Met Ala Ser Gly Phe Ser Lys Gly Pro Thr Leu Gly Leu				
	130	135	140	
ctg ccc gac gtg ccc tcc ctg atg gag aca ctc agc tac agc tac tgc				720
Leu Pro Asp Val Pro Ser Leu Met Glu Thr Leu Ser Tyr Ser Tyr Cys				
	145	150	155	
tac gtg gga atc atg aca ggc ccg ttc ttc cgc tac cgc acc tac ctg				768
Tyr Val Gly Ile Met Thr Gly Pro Phe Phe Arg Tyr Arg Thr Tyr Leu				
	160	165	170	
gac tgg ctg gag cag ccc ttc ccc ggg gca gtg ccc agc ctg cgg ccc				816
Asp Trp Leu Glu Gln Pro Phe Pro Gly Ala Val Pro Ser Leu Arg Pro				
	175	180	185	190
ctg ctg cgc cgc gcc tgg ccg gcc ccg ctc ttc ggc ctg ctg ttc ctg				864
Leu Leu Arg Arg Ala Trp Pro Ala Pro Leu Phe Gly Leu Leu Phe Leu				
	195	200	205	
ctc tcc tct cac ctc ttc ccg ctg gag gcc gtg cgc gag gac gcc ttc				912
Leu Ser Ser His Leu Phe Pro Leu Glu Ala Val Arg Glu Asp Ala Phe				
	210	215	220	
tac gcc cgc ccg ctg ccc gcc cgc ctc ttc tac atg atc ccc gtc ttc				960
Tyr Ala Arg Pro Leu Pro Ala Arg Leu Phe Tyr Met Ile Pro Val Phe				
	225	230	235	

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ttc gcc ttc cgc atg cgc ttc tac gtg gcc tgg att gcc gcc gag tgc 1008
 Phe Ala Phe Arg Met Arg Phe Tyr Val Ala Trp Ile Ala Ala Glu Cys
 240 245 250
 ggc tgc att gcc gcc ggc ttt ggg gcc tac ccc gtg gcc gcc aaa gcc 1056
 Gly Cys Ile Ala Ala Gly Phe Gly Ala Tyr Pro Val Ala Ala Lys Ala
 255 260 265 270
 cgg gcc gga ggc ggc ccc acc ctc caa tgc cca ccc ccc agc agt ccg 1104
 Arg Ala Gly Gly Gly Pro Thr Leu Gln Cys Pro Pro Pro Ser Ser Pro
 275 280 285
 gag aag gcg gct tcc ttg gag tat gac tat gag acc atc cgc aac atc 1152
 Glu Lys Ala Ala Ser Leu Glu Tyr Asp Tyr Glu Thr Ile Arg Asn Ile
 290 295 300
 gac tgc tac agc aca gat ttc tgc gtg cgg gtg cgc gat ggc atg cgg 1200
 Asp Cys Tyr Ser Thr Asp Phe Cys Val Arg Val Arg Asp Gly Met Arg
 305 310 315
 tac tgg aac atg acg gtg cag tgg tgg ctg gcg cag tat atc tac aag 1248
 Tyr Trp Asn Met Thr Val Gln Trp Trp Leu Ala Gln Tyr Ile Tyr Lys
 320 325 330
 agc gca cct gcc cgt tcc tat gtc ctg cgc ctt tagaagcaga aactcagcc 1300
 Ser Ala Pro Ala Arg Ser Tyr Val Leu Arg Leu
 335 340 345
 ggggtcggcg gctcacgcct ggaatcccag cactttggga ggcccaagca ggtggatcat 1360
 gaggagcgcc tggaccatgc tgctgagcgc ctactggcac ggctccacc cgggctacta 1420
 cctgagcttc ctgaccatcc cgctgtgcct ggctgccgag ggccggctgg agtcagccct 1480
 gcgggggcgg ctgagcccag ggggccagaa ggccctgggac tgggtgcact ggttcctgaa 1540

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gatgcgcgcc tatgactaca tgtgcatggg ctctgtgctg ctctccttgg ccgacaccct 1600
tcggtactgg gcctccatct acttctgtat ccacttcctg gccctggcag ccctggggct 1660
ggggctggct ttaggtgggg gcagccccag ccggcggaag gcagcatccc agcccaccag 1720
ccttgccccg gagaagctcc gggaggagta agctgtcacg acgctccctc tgccagctgg 1780
tcccgggaat tctgtgaacc aggtctgtgt ctctcccca gaaagagtcc ttaccttgga 1840
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acccgggggt gtctccctg cctctgtccc agaggccacc tccactccta caaaatcaaa 1960
gtattgtcca gacaagagtc actggcccct gtccagctt ctgggtatcc agagagcact 2020
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tgcatccaca atgtggggtc ggagcttggg ggcaggtcct gggagtggga agcctcttcc 2140
ttgtgtcttt cgtccactt ttagctcatc gcaccaatat tgcagacttg gaaggaagca 2200
taagcttccc atttcacaaa ggggaaactg aggtgcgggt gcgcgggcct ggggacggcc 2260
gtcccatggc ttccatctga gccacctcg gacccagca ctcttggcgc cctcttctca 2320
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<210> 28

<211> 2017

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (360)... (629)

<400> 28

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tgagaatgaa tctgacctca gacccaaatc cattcaacgg agttctggta atttgaaga 120

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aggaagagca acctggaaac tgacaggaaa ggatgacaag ttgggagtca caggatatatg 180
 atgggcctcc ccatgtggat ccttagtgct gtggcagagc ccttggtatt gtgctgggat 240
 ttccctcca gctcccgcc ggaagctggg ctcacgtggg agctcagtgc cctcctgcta 300
 cagatctgtc tcttccttac aatgggggtgc tggcactgtg ggtcctggtg acgcacgtg 359
 atg tac atg caa gat tat tgg agg acc tgg ctc aag ggg ctg cgc ggc 407
 Met Tyr Met Gln Asp Tyr Trp Arg Thr Trp Leu Lys Gly Leu Arg Gly
 1 5 10 15
 ttc ttc ttc gtg ggc gtc ctc ttc tgg gcc gtc tcc atc gct gcc ttc 455
 Phe Phe Phe Val Gly Val Leu Phe Ser Ala Val Ser Ile Ala Ala Phe
 20 25 30
 tgc acc ttc ctc gtg ctg gcc atc acc cgg cat cag agc ctc aca gac 503
 Cys Thr Phe Leu Val Leu Ala Ile Thr Arg His Gln Ser Leu Thr Asp
 35 40 45
 ccc acc agc tac tac ctc tcc agc gtc tgg agc ttc att tcc ttc aag 551
 Pro Thr Ser Tyr Tyr Leu Ser Ser Val Trp Ser Phe Ile Ser Phe Lys
 50 55 60
 tgg gcc ttc ctg ctc agc ctc tat gcc cac cgc tac cgg gct gac ttt 599
 Trp Ala Phe Leu Leu Ser Leu Tyr Ala His Arg Tyr Arg Ala Asp Phe
 65 70 75 80
 gct gac atc agc atc ctc agc gat ttc tgaccaggg ggtg 640
 Ala Asp Ile Ser Ile Leu Ser Asp Phe
 85
 aggtctctgc acctggggg ggccttagga cctggactca gcctctgaga tgttgggaga 700
 ggctactccc acccctggt gacccagaa ctgtggcaga aaatacacag caggacgagt 760
 gtggtctccc aggaagctgt cctgccgctc ccctttcgag gaaacctgag tgtggtagag 820

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aggggatcct gccatgttgt tcctcatcag cctggccaga gggcagcttt agaccttttc 880
 aaatgaatct gttttctttt ctttctttt ttttctttt tttttttt ttgagatgga 940
 gtcttactct gtcaccacagg ctggagtgca gtagtgcat ctcagctcac tgcaacctcc 1000
 gcctcccagg ttcaagcaat tctcctgcct tggcctctca agtagctggg attacaggca 1060
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 aggccctggac ctatgtgca ggcaagggtt tccatccccg ctgccctagg cactctcttc 1360
 ccaaggccag gttgggcacc tggggaggtc agttcagaaa tatctagcag agacctctta 1420
 aacccccatc ccagcaccac atcctgttgt tcccagagct ggtctcccat gagtgtgcta 1480
 gagccagata gccgtggccc cccaccatc tcactcacac acacaggcat ccatacacc 1540
 cagaagactt cccaatgag gccagactca gggtcacggg gaatgtgctt ctgccctgt 1600
 aagggtttg gggaaggggg caacatagta gaggttgaa agagccccc aacctgtgcc 1660
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 accaccggcc aggagagacc ttctctccca ctccagcccc tctcactgcc cttcaactag 1780
 agctttcacc tttttacatt tcccttctga aggacacaaa tctgcttttc tgccataca 1840
 ctggcccaag ggctcaccta acttgggagg gaaggggctg ttggtacaag gatgattttc 1900
 tgttagactg ccattttgca cggctctccc ctcccatct gatgtgtcct gccctcagc 1960
 tctttgcctt atctgtgtca ctgtcacttt agcaaaaata cagcgccat ttgtatc 2017

<210> 29

<211> 1606

<212> DNA

<213> Homo sapiens

61 / 307

<220>

<221> CDS.

<222> (30)... (1250)

<400> 29

acctcttcg tcggctgaat tgcggccgt atg cgc ggc tct gtg gag tgc acc 53

Met Arg Gly Ser Val Glu Cys Thr

1

5

tgg ggt tgg ggg cac tgt gcc ccc agc ccc ctg ctc ctt tgg act cta 101

Trp Gly Trp Gly His Cys Ala Pro Ser Pro Leu Leu Leu Trp Thr Leu

10

15

20

ctt ctg ttt gca gcc cca ttt ggc ctg ctg ggg gag aag acc cgc cag 149

Leu Leu Phe Ala Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr Arg Gln

25

30

35

40

gtg tct ctg gag gtc atc cct aac tgg ctg ggc ccc ctg cag aac ctg 197

Val Ser Leu Glu Val Ile Pro Asn Trp Leu Gly Pro Leu Gln Asn Leu

45

50

55

ctt cat ata cgg gca gtg ggc acc aat tcc aca ctg cac tat gtg tgg 245

Leu His Ile Arg Ala Val Gly Thr Asn Ser Thr Leu His Tyr Val Trp

60

65

70

agc agc ctg ggg cct ctg gca gtg gta atg gtg gcc acc aac acc ccc 293

Ser Ser Leu Gly Pro Leu Ala Val Val Met Val Ala Thr Asn Thr Pro

75

80

85

cac agc acc ctg agc gtc aac tgg agc ctc ctg cta tcc cct gag ccc 341

His Ser Thr Leu Ser Val Asn Trp Ser Leu Leu Leu Ser Pro Glu Pro

90

95

100

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gat ggg ggc ctg atg gtg ctc cct aag gac agc att cag ttt tct tct 389
 Asp Gly Gly Leu Met Val Leu Pro Lys Asp Ser Ile Gln Phe Ser Ser
 105 110 115 120
 gcc ctt gtt ttt acc agg ctg ctt gag ttt gac agc acc aac gtg tcc 437
 Ala Leu Val Phe Thr Arg Leu Leu Glu Phe Asp Ser Thr Asn Val Ser
 125 130 135
 gat acg gca gca aag cct ttg gga aga cca tat cct cca tac tcc ttg 485
 Asp Thr Ala Ala Lys Pro Leu Gly Arg Pro Tyr Pro Pro Tyr Ser Leu
 140 145 150
 gcc gat ttc tct tgg aac aac atc act gat tca ttg gat cct gcc acc 533
 Ala Asp Phe Ser Trp Asn Asn Ile Thr Asp Ser Leu Asp Pro Ala Thr
 155 160 165
 ctg agt gcc aca ttt caa ggc cac ccc atg aac gac cct acc agg act 581
 Leu Ser Ala Thr Phe Gln Gly His Pro Met Asn Asp Pro Thr Arg Thr
 170 175 180
 ttt gcc aat ggc agc ctg gcc ttc agg gtc cag gcc ttt tcc agg tcc 629
 Phe Ala Asn Gly Ser Leu Ala Phe Arg Val Gln Ala Phe Ser Arg Ser
 185 190 195 200
 agc cga cca gcc caa ccc cct cgc ctc ctg cac aca gca gac acc tgt 677
 Ser Arg Pro Ala Gln Pro Pro Arg Leu Leu His Thr Ala Asp Thr Cys
 205 210 215
 cag cta gag gtg gcc ctg att gga gcc tct ccc cgg gga aac cgt tcc 725
 Gln Leu Glu Val Ala Leu Ile Gly Ala Ser Pro Arg Gly Asn Arg Ser
 220 225 230
 ctg ttt ggg ctg gag gta gcc aca ttg ggc cag ggc cct gac tgc ccc 773

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Leu Phe Gly Leu Glu Val Ala Thr Leu Gly Gln Gly Pro Asp Cys Pro
 235 240 245
 tca atg cag gag cag cac tcc atc gac gat gaa tat gca ccg gcc gtc 821
 Ser Met Gln Glu Gln His Ser Ile Asp Asp Glu Tyr Ala Pro Ala Val
 250 255 260
 ttc cag ttg gac cag cta ctg tgg ggc tcc ctc cca tca ggc ttt gca 869
 Phe Gln Leu Asp Gln Leu Leu Trp Gly Ser Leu Pro Ser Gly Phe Ala
 265 270 275 280
 cag tgg cga cca gtg gct tac tcc cag aag ccg ggg ggc cga gaa tca 917
 Gln Trp Arg Pro Val Ala Tyr Ser Gln Lys Pro Gly Gly Arg Glu Ser
 285 290 295
 gcc ctg ccc tgc caa gct tcc cct ctt cat cct gcc tta gca tac tct 965
 Ala Leu Pro Cys Gln Ala Ser Pro Leu His Pro Ala Leu Ala Tyr Ser
 300 305 310
 ctt ccc cag tca ccc att gtc cga gcc ttc ttt ggg tcc cag aat aac 1013
 Leu Pro Gln Ser Pro Ile Val Arg Ala Phe Phe Gly Ser Gln Asn Asn
 315 320 325
 ttc tgt gcc ttc aat ctg acg ttc ggg gct tcc aca ggc cct ggc tat 1061
 Phe Cys Ala Phe Asn Leu Thr Phe Gly Ala Ser Thr Gly Pro Gly Tyr
 330 335 340
 tgg gac caa cac tac ctc agc tgg tcg atg ctc ctg ggt gtg ggc ttc 1109
 Trp Asp Gln His Tyr Leu Ser Trp Ser Met Leu Leu Gly Val Gly Phe
 345 350 355 360
 cct cca gtg gac ggc ttg tcc cca cta gtc ctg ggc atc atg gca gtg 1157
 Pro Pro Val Asp Gly Leu Ser Pro Leu Val Leu Gly Ile Met Ala Val

64 /307

365 370 375
gcc ctg ggt gcc cca ggg ctc atg ctg cta ggg ggc ggc ttg gtt ctg 1205
Ala Leu Gly Ala Pro Gly Leu Met Leu Leu Gly Gly Gly Leu Val Leu
380 385 390
ctg ctg cac cac aag aag tac tca gag tac cag tcc ata aat taa 1250
Leu Leu His His Lys Lys Tyr Ser Glu Tyr Gln Ser Ile Asn
395 400 405
ggcccgtct ctggaggga gacattact gaacctgtct tgctgtgcct cgaaactctg 1310
gaggttgag catcaagtc cagcggccc cttcactccc ccatcttget tttctgtgga 1370
acctcagagg ccagcctcga cttcctggag acccccaggt ggggttcct tcatactttg 1430
ttgggggact ttggaggcgg gcaggggaca gggctattga taaggctccc ttggtgttgc 1490
cttcttgcac ctccacacat ttcccttggga tgggacttgc aggcctaat gagaggcatt 1550
ctgactggtt ggctgcctg gaaggcaaga aaatagattt attttttttc acaggg 1606

<210> 30

<211> 1695

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)... (631)

<400> 30

acagccgagc agctggagcg atcgaggctg cagcgcggcc gccgggcgca gc atg 55

Met

65 /307

act gcc gtc ggc gtg cag gcc cag agg cct ttg ggc caa agg cag ccc 103
 Thr Ala Val Gly Val Gln Ala Gln Arg Pro Leu Gly Gln Arg Gln Pro
 5 10 15

cgc cgg tcc ttc ttt gaa tcc ttc atc cgg acc ctc atc atc acg tgt 151
 Arg Arg Ser Phe Phe Glu Ser Phe Ile Arg Thr Leu Ile Ile Thr Cys
 20 25 30

gtg gcc ctg gct gtg gtc ctg tcc tcg gtc tcc att tgt gat ggg cac 199
 Val Ala Leu Ala Val Val Leu Ser Ser Val Ser Ile Cys Asp Gly His
 35 40 45

tgg ctc ctg gct gag gac cgc ctc ttc ggg ctc tgg cac ttc tgc acc 247
 Trp Leu Leu Ala Glu Asp Arg Leu Phe Gly Leu Trp His Phe Cys Thr
 50 55 60 65

acc acc aac cag agt gtg ccg atc tgc ttc aga gac ctg ggc cag gcc 295
 Thr Thr Asn Gln Ser Val Pro Ile Cys Phe Arg Asp Leu Gly Gln Ala
 70 75 80

cat gtg ccc ggg ctg gcc gtg ggc atg ggc ctg gta cgc agc gtg ggc 343
 His Val Pro Gly Leu Ala Val Gly Met Gly Leu Val Arg Ser Val Gly
 85 90 95

gcc ttg gcc gtg gtg gcc gcc att ttt ggc ctg gag ttc ctc atg gtg 391
 Ala Leu Ala Val Val Ala Ala Ile Phe Gly Leu Glu Phe Leu Met Val
 100 105 110

tcc cag ttg tgc gag gac aaa cac tca cag tgc aag tgg gtc atg ggt 439
 Ser Gln Leu Cys Glu Asp Lys His Ser Gln Cys Lys Trp Val Met Gly
 115 120 125

tcc atc ctc ctc ctg gtg tct ttc gtc ctc tcc tcc ggc ggc ctc ctg 487

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Ser Ile Leu Leu Leu Val Ser Phe Val Leu Ser Ser Gly Gly Leu Leu
 130 135 140 145
 ggt ttt gtg atc ctc ctc agg aac caa gtc aca ctc atc ggc ttc acc 535
 Gly Phe Val Ile Leu Leu Arg Asn Gln Val Thr Leu Ile Gly Phe Thr
 150 155 160
 cta atg ttt tgg tgc gaa ttc act gcc tcc ttc ctc ctc ttc ctg aac 583
 Leu Met Phe Trp Cys Glu Phe Thr Ala Ser Phe Leu Leu Phe Leu Asn
 165 170 175
 gcc atc agc ggc ctt cac atc aac agc atc acc cat ccc tgg gaa tg 630
 Ala Ile Ser Gly Leu His Ile Asn Ser Ile Thr His Pro Trp Glu
 180 185 190
 accgtggaaa ttttaggccc cctccaggga catcagattc cacaagaaaa tatgggtcaaa 690
 atgggacttt tccagcatgt ggccctctggt ggggctgggt tggacaaggc ccttgaaacg 750
 gctgcctgtt tgccgataac ttgtgggtgg tcagccagaa atggcccggg ggccctctgca 810
 cctggtctgc agggccagag gccaggaggg tgcctcagt ccaccaactg cacaggctta 870
 gccagatgtt gatcttagag gaagaaaaaa acattttaaa actccttctt gaattttctt 930
 ccctggactg gaatacagtt ggaagcacag gggttaactg tacctgagct agctgcacag 990
 ccaaggatag ttcatgcctg ttccattgac acgtgctggg ataggggctg cagaatccct 1050
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 attcttcac cagctcaaag ggccctcgta tgtatgtccc tggcttcagc tttggtcatg 1170
 ccaaagaggc agagttcagg attccctcag aatgccctgc acacagtagg ttccaaacc 1230
 atttgactcg gtttgctcc ctgccgttg tttaaacctt acaaaccctg gataacccca 1290
 tcttctagca gctggctgtc ccctctggga gctctgccta tcagaaccct accttaagg 1350
 gggtttcctt ccgagaagag ttcttgagca agctctccca ggagggccca cctgactgct 1410
 aatacacagc cctccccaag gcccggtgtg gcattgtgtc gtcttttgtg aggggttagac 1470

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agcctcaggg caccattttt aatcccagaa cacatttcaa agagcacgta tctagacctg 1530
 ctggactctg caggggggtga gggggaacag cgagagcttg ggtaatgatt aacacccatg 1590
 ctgggggatgc atggaggtga agggggccag gaaccagtgg agatttccat ccttgccagc 1650
 acgtctgtac ttctgttcat taaagtgtc cctttctagt ccttt 1695

<210> 31

<211> 377

<212> PRT

<213> Homo sapiens

<400> 31

Met Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly

1 5 10 15

Gly Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile

20 25 30

Ala Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe

35 40 45

Phe Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser

50 55 60

Asp Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile

65 70 75 80

Ile Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe

85 90 95

Ser Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu

100 105 110

Gly Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe

68 / 307

115 120 125
Phe Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln
130 135 140
Gly Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr
145 150 155 160
Lys Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr
165 170 175
Leu Leu Arg Lys His Trp Ile Ala Asn Asn Leu Phe Gly Leu Ala Phe
180 185 190
Ser Leu Asn Gly Val Glu Leu Leu His Leu Asn Asn Val Ser Thr Gly
195 200 205
Cys Ile Leu Leu Gly Gly Leu Phe Ile Tyr Asp Val Phe Trp Val Phe
210 215 220
Gly Thr Asn Val Met Val Thr Val Ala Lys Ser Phe Glu Ala Pro Ile
225 230 235 240
Lys Leu Val Phe Pro Gln Asp Leu Leu Glu Lys Gly Leu Glu Ala Asn
245 250 255
Asn Phe Ala Met Leu Gly Leu Gly Asp Val Val Ile Pro Gly Ile Phe
260 265 270
Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser Leu Lys Lys Asn Thr His
275 280 285
Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr Ile Phe Gly Leu Gly Leu
290 295 300
Thr Ile Phe Ile Met His Ile Phe Lys His Ala Gln Pro Ala Leu Leu
305 310 315 320

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Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro Val Leu Val Ala Leu Ala

325

330

335

Lys Gly Glu Val Thr Glu Met Phe Ser Tyr Glu Glu Ser Asn Pro Lys

340

345

350

Asp Pro Ala Ala Val Thr Glu Ser Lys Glu Gly Thr Glu Ala Ser Ala

355

360

365

Ser Lys Gly Leu Glu Lys Lys Glu Lys

370

375

<210> 32

<211> 81

<212> PRT

<213> Homo sapiens

<400> 32

Met Thr Ala His Ser Phe Ala Leu Pro Val Ile Ile Phe Thr Thr Phe

1

5

10

15

Trp Gly Leu Val Gly Ile Ala Gly Pro Trp Phe Val Pro Lys Gly Pro

20

25

30

Asn Arg Gly Val Ile Ile Thr Met Leu Val Ala Thr Ala Val Cys Cys

35

40

45

Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu Asn Pro Leu Phe

50

55

60

Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Val Arg Phe Leu Trp

65

70

75

80

Glu

70 / 307

<210> 33

<211> 487

<212> PRT

<213> Homo sapiens

<400> 33

Met Gly Asp Thr Gly Leu Arg Lys Arg Arg Glu Asp Glu Lys Ser Ile

1 5 10 15

Gln Ser Gln Glu Pro Lys Thr Thr Ser Leu Gln Lys Glu Leu Gly Leu

20 25 30

Ile Ser Gly Ile Ser Ile Ile Val Gly Thr Ile Ile Gly Ser Gly Ile

35 40 45

Phe Val Ser Pro Lys Ser Val Leu Ser Asn Thr Glu Ala Val Gly Pro

50 55 60

Cys Leu Ile Ile Trp Ala Ala Cys Gly Val Leu Ala Thr Leu Gly Ala

65 70 75 80

Leu Cys Phe Ala Glu Leu Gly Thr Met Ile Thr Lys Ser Gly Gly Glu

85 90 95

Tyr Pro Tyr Leu Met Glu Ala Tyr Gly Pro Ile Pro Ala Tyr Leu Phe

100 105 110

Ser Trp Ala Ser Leu Ile Val Ile Lys Pro Thr Ser Phe Ala Ile Ile

115 120 125

Cys Leu Ser Phe Ser Glu Tyr Val Cys Ala Pro Phe Tyr Val Gly Cys

130 135 140

71 / 307

Lys Pro Pro Gln Ile Val Val Lys Cys Leu Ala Ala Ala Ala Ile Leu

145 150 155 160

Phe Ile Ser Thr Val Asn Ser Leu Ser Val Arg Leu Gly Ser Tyr Val

165 170 175

Gln Asn Ile Phe Thr Ala Ala Lys Leu Val Ile Val Ala Ile Ile Ile

180 185 190

Ile Ser Gly Leu Val Leu Leu Ala Gln Gly Asn Thr Lys Asn Phe Asp

195 200 205

Asn Ser Phe Glu Gly Ala Gln Leu Ser Val Gly Ala Ile Ser Leu Ala

210 215 220

Phe Tyr Asn Gly Leu Trp Ala Tyr Asp Gly Trp Asn Gln Leu Asn Tyr

225 230 235 240

Ile Thr Glu Glu Leu Arg Asn Pro Tyr Arg Asn Leu Pro Leu Ala Ile

245 250 255

Ile Ile Gly Ile Pro Leu Val Thr Ala Cys Tyr Ile Leu Met Asn Val

260 265 270

Ser Tyr Phe Thr Val Met Thr Ala Thr Glu Leu Leu Gln Ser Gln Ala

275 280 285

Val Ala Val Thr Phe Gly Asp Arg Val Leu Tyr Pro Ala Ser Trp Ile

290 295 300

Val Pro Leu Phe Val Ala Phe Ser Thr Ile Gly Ala Ala Asn Gly Thr

305 310 315 320

Cys Phe Thr Ala Gly Arg Leu Ile Tyr Val Ala Gly Arg Glu Gly His

325 330 335

Met Leu Lys Val Leu Ser Tyr Ile Ser Val Arg Arg Leu Thr Pro Ala

72 / 307

340 345 350
Pro Ala Ile Ile Phe Tyr Gly Ile Ile Ala Thr Ile Tyr Ile Ile Pro
355 360 365
Gly Asp Ile Asn Ser Leu Val Asn Tyr Phe Ser Phe Ala Ala Trp Leu
370 375 380
Phe Tyr Gly Leu Thr Ile Leu Gly Leu Ile Val Met Arg Phe Thr Arg
385 390 395 400
Lys Glu Leu Glu Arg Pro Ile Lys Val Pro Val Val Ile Pro Val Leu
405 410 415
Met Thr Leu Ile Ser Val Phe Leu Val Leu Ala Pro Ile Ile Ser Lys
420 425 430
Pro Thr Trp Glu Tyr Leu Tyr Cys Val Leu Phe Ile Leu Ser Gly Leu
435 440 445
Leu Phe Tyr Phe Leu Phe Val His Tyr Lys Phe Gly Trp Ala Gln Lys
450 455 460
Ile Ser Lys Pro Ile Thr Met His Leu Gln Met Leu Met Glu Val Val
465 470 475 480
Pro Pro Glu Glu Asp Pro Glu
485

<210> 34

<211> 375

<212> PRT

<213> Homo sapiens

<400> 34

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Met Thr Pro Gln Pro Ala Gly Pro Pro Asp Gly Gly Trp Gly Trp Val

1 5 10 15

Val Ala Ala Ala Ala Phe Ala Ile Asn Gly Leu Ser Tyr Gly Leu Leu

20 25 30

Arg Ser Leu Gly Leu Ala Phe Pro Asp Leu Ala Glu His Phe Asp Arg

35 40 45

Ser Ala Gln Asp Thr Ala Trp Ile Ser Ala Leu Ala Leu Ala Val Gln

50 55 60

Gln Ala Ala Ser Pro Val Gly Ser Ala Leu Ser Thr Arg Trp Gly Ala

65 70 75 80

Arg Pro Val Val Met Val Gly Gly Val Leu Ala Ser Leu Gly Phe Val

85 90 95

Phe Ser Ala Phe Ala Ser Gly Leu Leu His Leu Tyr Leu Gly Leu Gly

100 105 110

Leu Leu Ala Gly Phe Gly Trp Ala Leu Val Phe Ala Pro Ala Leu Gly

115 120 125

Thr Leu Ser Arg Tyr Phe Ser Arg Arg Arg Val Leu Ala Val Gly Leu

130 135 140

Ala Leu Thr Gly Asn Gly Ala Ser Ser Leu Leu Leu Ala Pro Ala Leu

145 150 155 160

Gln Leu Leu Leu Asp Thr Phe Gly Trp Arg Gly Ala Leu Leu Leu Leu

165 170 175

Gly Ala Ile Thr Leu His Leu Thr Pro Cys Gly Ala Leu Leu Leu Pro

180 185 190

Leu Val Leu Pro Gly Asp Pro Pro Ala Pro Pro Arg Ser Pro Leu Ala

74 /307

195 200 205
Ala Leu Gly Leu Ser Leu Phe Thr Arg Arg Ala Phe Ser Ile Phe Ala
210 215 220
Leu Gly Thr Ala Leu Val Gly Gly Gly Tyr Phe Val Pro Tyr Val His
225 230 235 240
Leu Ala Pro Arg Phe Arg Pro Gly Pro Gly Gly Ile Arg Ser Ser Ala
245 250 255
Gly Gly Gly Arg Gly Cys Asp Gly Gly Cys Gly Arg Pro Ala Gly Leu
260 265 270
Arg Val Ala Gly Arg Pro Arg Leu Gly Ala Pro Pro Ala Ala Ala Gly
275 280 285
Arg Ile Arg Gly Ser Asp Trp Ala Gly Ala Val Gly Gly Gly Ala Gly
290 295 300
Ala Arg Gly Gly Arg Arg Arg Glu Leu Gly Gly Ser Pro Ala Gly Arg
305 310 315 320
Gly Cys Gly Leu Trp Ala Glu Arg Gly Glu Leu Arg Pro Ala Gly Phe
325 330 335
Arg Cys Thr Pro Arg Ala Gly Gly Arg Arg Arg Cys Gly Ala Gly His
340 345 350
Arg Ala Gly Asp Asp Ala Asp Glu Pro Arg Gly Ala Pro Gly Pro Ser
355 360 365
Pro Val Arg Leu Pro Lys Gly
370 375

<210> 35

75 / 307

<211> 350

<212> PRT

<213> Homo sapiens

<400> 35

Met Ala Thr Thr Ala Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly

1 5 10 15

Pro Glu Trp Gly Gly Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala

20 25 30

Val Ile Asp Met Glu Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu

35 40 45

Asp Met Gly Glu Leu His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala

50 55 60

Asp Ala Ala Asp Ala Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu

65 70 75 80

Gly Met Lys Gly Phe Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln

85 90 95

Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr

100 105 110

Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln

115 120 125

Val Arg Ser Arg Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn

130 135 140

Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val

145 150 155 160

Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr

76 / 307

165 170 175
Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe
180 185 190
Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu
195 200 205
Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr
210 215 220
Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His
225 230 235 240
Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser
245 250 255
Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr
260 265 270
Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe
275 280 285
Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu
290 295 300
Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg
305 310 315 320
Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu
325 330 335
Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His
340 345 350
<210> 36

77 / 307

<211> 667

<212> PRT

<213> Homo sapiens

<400> 36

Met Ser Ser Gln Pro Ala Gly Asn Gln Thr Ser Pro Gly Ala Thr Glu

1 5 10 15

Asp Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu Pro Gln Gly Gly Glu

20 25 30

Glu Leu Gln Pro Glu Gly Glu Val Pro Ser Cys His Thr Ser Ile Pro

35 40 45

Pro Gly Leu Tyr His Ala Cys Leu Ala Ser Leu Ser Ile Leu Val Leu

50 55 60

Leu Leu Leu Ala Met Leu Val Arg Arg Arg Gln Leu Trp Pro Asp Cys

65 70 75 80

Val Arg Gly Arg Pro Gly Leu Pro Ser Pro Val Asp Phe Leu Ala Gly

85 90 95

Asp Arg Pro Arg Ala Val Pro Ala Ala Val Phe Met Val Leu Leu Ser

100 105 110

Ser Leu Cys Leu Leu Leu Pro Asp Glu Asp Ala Leu Pro Phe Leu Thr

115 120 125

Leu Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr Glu Ala Pro Arg Gly

130 135 140

Ala Trp Lys Ile Leu Gly Leu Phe Tyr Tyr Ala Ala Leu Tyr Tyr Pro

145 150 155 160

Leu Ala Ala Cys Ala Thr Ala Gly His Thr Ala Ala His Leu Leu Gly

78 / 307

165 170 175
Ser Thr Leu Ser Trp Ala His Leu Gly Val Gln Val Trp Gln Arg Ala
180 185 190
Glu Cys Pro Gln Val Pro Lys Ile Tyr Lys Tyr Tyr Ser Leu Leu Ala
195 200 205
Ser Leu Pro Leu Leu Leu Gly Leu Gly Phe Leu Ser Leu Trp Tyr Pro
210 215 220
Val Gln Leu Val Arg Ser Phe Ser Arg Arg Thr Gly Ala Gly Ser Lys
225 230 235 240
Gly Leu Gln Ser Ser Tyr Ser Glu Glu Tyr Leu Arg Asn Leu Leu Cys
245 250 255
Arg Lys Lys Leu Gly Ser Ser Tyr His Thr Ser Lys His Gly Phe Leu
260 265 270
Ser Trp Ala Arg Val Cys Leu Arg His Cys Ile Tyr Thr Pro Gln Pro
275 280 285
Gly Phe His Leu Pro Leu Lys Leu Val Leu Ser Ala Thr Leu Thr Gly
290 295 300
Thr Ala Ile Tyr Gln Val Ala Leu Leu Leu Leu Val Gly Val Val Pro
305 310 315 320
Thr Ile Gln Lys Val Arg Ala Gly Val Thr Thr Asp Val Ser Tyr Leu
325 330 335
Leu Ala Gly Phe Gly Ile Val Leu Ser Glu Asp Lys Gln Glu Val Val
340 345 350
Glu Leu Val Lys His His Leu Trp Ala Leu Glu Val Cys Tyr Ile Ser
355 360 365

79 / 307

Ala Leu Val Leu Ser Cys Leu Leu Thr Phe Leu Val Leu Met Arg Ser
 370 375 380
 Leu Val Thr His Arg Thr Asn Leu Arg Ala Leu His Arg Gly Ala Ala
 385 390 395 400
 Leu Asp Leu Ser Pro Leu His Arg Ser Pro His Pro Ser Arg Gln Ala
 405 410 415
 Ile Phe Cys Trp Met Ser Phe Ser Ala Tyr Gln Thr Ala Phe Ile Cys
 420 425 430
 Leu Gly Leu Leu Val Gln Gln Ile Ile Phe Phe Leu Gly Thr Thr Ala
 435 440 445
 Leu Ala Phe Leu Val Leu Met Pro Val Leu His Gly Arg Asn Leu Leu
 450 455 460
 Leu Phe Arg Ser Leu Glu Ser Ser Trp Pro Phe Trp Leu Thr Leu Ala
 465 470 475 480
 Leu Ala Val Ile Leu Gln Asn Met Ala Ala His Trp Val Phe Leu Glu
 485 490 495
 Thr His Asp Gly His Pro Gln Leu Thr Asn Arg Arg Val Leu Tyr Ala
 500 505 510
 Ala Thr Phe Leu Leu Phe Pro Leu Asn Val Leu Val Gly Ala Met Val
 515 520 525
 Ala Thr Trp Arg Val Leu Leu Ser Ala Leu Tyr Asn Ala Ile His Leu
 530 535 540
 Gly Gln Met Asp Leu Ser Leu Leu Pro Pro Arg Ala Ala Thr Leu Asp
 545 550 555 560
 Pro Gly Tyr Tyr Thr Tyr Arg Asn Phe Leu Lys Ile Glu Val Ser Gln

565

575

580

585

590

595

600

605

610

615

620

625 '

630

635

640

645

650

655

660

665

<211> 464

<212> PRT

<213> Homo sapiens

<400> 37

1

5

- 10

15

20

25

30

35

40

45

81 / 307

Val Leu Ser Tyr Phe Ser Ser His Tyr Pro Pro Ser Ile Ile Leu Ala
50 55 60
Lys Glu Ser Tyr Ala Glu Leu Ile Met Lys Leu Leu Lys Val Ser Ala
65 70 75 80
Gly Leu Ser Ile Pro Thr Asp Ser Gln Lys His Leu Asp Ala Val Pro
85 90 95
Lys Cys Gln Ala Phe Thr His Gln Met Val Gln Phe Leu Ser Thr Leu
100 105 110
Glu Gln Asn Gly Lys Ile Thr Leu Ala Val Leu Glu Gln Glu Met Ser
115 120 125
Lys Leu Leu Asp Asp Ile Ile Val Phe Asn Pro Pro Asp Met Asp Ser
130 135 140
Gln Thr Arg His Met Ala Leu Ser Ser Leu Phe Met Glu Val Leu Met
145 150 155 160
Met Met Asn Asn Ala Thr Ile Pro Thr Ala Glu Phe Leu Arg Gly Ser
165 170 175
Ile Arg Thr Trp Ile Gly Gln Lys Met His Gly Leu Val Val Leu Pro
180 185 190
Leu Leu Thr Ala Ala Cys Gln Ser Leu Ala Ser Val Arg His Met Ala
195 200 205
Glu Thr Thr Glu Ala Cys Ile Thr Ala Tyr Phe Lys Glu Ser Pro Leu
210 215 220
Asn Gln Asn Ser Gly Trp Gly Pro Ile Leu Val Ser Leu Gln Val Pro
225 230 235 240
Glu Leu Thr Met Glu Glu Phe Leu Gln Glu Cys Leu Thr Leu Gly Ser

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245 250 255
Tyr Leu Thr Leu Tyr Val Tyr Leu Leu Gln Cys Leu Asn Ser Glu Gln
260 265 270
Thr Leu Arg Asn Glu Met Lys Val Leu Leu Ile Leu Ser Lys Trp Leu
275 280 285
Glu Gln Val Tyr Pro Ser Ser Val Glu Glu Glu Ala Lys Leu Phe Leu
290 295 300
Trp Trp His Gln Val Leu Gln Leu Ser Leu Ile Gln Thr Glu Gln Asn
305 310 315 320
Asp Ser Val Leu Thr Glu Ser Val Ile Arg Ile Leu Leu Leu Val Gln
325 330 335
Ser Arg Gln Asn Leu Val Ala Glu Glu Arg Leu Ser Ser Gly Ile Leu
340 345 350
Gly Ala Ile Gly Phe Gly Arg Lys Ser Pro Leu Ser Asn Arg Phe Arg
355 360 365
Val Val Ala Arg Ser Met Ala Ala Phe Leu Ser Val Gln Val Pro Met
370 375 380
Glu Asp Gln Ile Arg Leu Arg Pro Gly Ser Glu Leu His Leu Thr Pro
385 390 395 400
Lys Ala Gln Gln Ala Leu Asn Ala Leu Glu Ser Met Ala Ser Ser Lys
405 410 415
Gln Tyr Val Glu Tyr Gln Asp Gln Ile Leu Gln Ala Thr Gln Phe Ile
420 425 430
Arg His Pro Gly His Cys Leu Gln Asp Gly Lys Ser Phe Leu Ala Leu
435 440 445

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Leu Val Asn Cys Leu Tyr Pro Glu Val His Tyr Leu Asp His Ile Arg

450

455

460

<210> 38

<211> 470

<212> PRT

<213> Homo sapiens

<400> 38

Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu

1

5

10

15

Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser

20

25

30

Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro

35

40

45

Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met

50

55

60

Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro

65

70

75

80

Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe

85

90

95

Val Leu Thr Ser Leu Val Ala Leu Arg Arg Glu Val Glu Glu Leu Arg

100

105

110

Ser Ser Leu Arg Gly Leu Ala Gly Glu Ile Val Gly Glu Val Arg Cys

115

120

125

His Met Glu Glu Asn Gln Arg Val Ala Arg Arg Arg Arg Phe Pro Phe

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130 135 140
Val Arg Glu Arg Ser Asp Ser Thr Gly Ser Ser Ser Val Tyr Phe Thr
145 150 155 160
Ala Ser Ser Gly Ala Thr Phe Thr Asp Ala Glu Ser Glu Gly Gly Tyr
165 170 175
Thr Thr Ala Asn Ala Glu Ser Asp Asn Glu Arg Asp Ser Asp Lys Glu
180 185 190
Ser Glu Asp Gly Glu Asp Glu Val Ser Cys Glu Thr Val Lys Met Gly
195 200 205
Arg Lys Asp Ser Leu Asp Leu Glu Glu Glu Ala Ala Ser Gly Ala Ser
210 215 220
Ser Ala Leu Glu Ala Gly Gly Ser Ser Gly Leu Glu Asp Val Leu Pro
225 230 235 240
Leu Leu Gln Gln Ala Asp Glu Leu His Arg Gly Asp Glu Gln Gly Lys
245 250 255
Arg Glu Gly Phe Gln Leu Leu Leu Asn Asn Lys Leu Val Tyr Gly Ser
260 265 270
Arg Gln Asp Phe Leu Trp Arg Leu Ala Arg Ala Tyr Ser Asp Met Cys
275 280 285
Glu Leu Thr Glu Glu Val Ser Glu Lys Lys Ser Tyr Ala Leu Asp Gly
290 295 300
Lys Glu Glu Ala Glu Ala Ala Leu Glu Lys Gly Asp Glu Ser Ala Asp
305 310 315 320
Cys His Leu Trp Tyr Ala Val Leu Cys Gly Gln Leu Ala Glu His Glu
325 330 335

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Ser Ile Gln Arg Arg Ile Gln Ser Gly Phe Ser Phe Lys Glu His Val

340

345

350

Asp Lys Ala Ile Ala Leu Gln Pro Glu Asn Pro Met Ala His Phe Leu

355

360

365

Leu Gly Arg Trp Cys Tyr Gln Val Ser His Leu Ser Trp Leu Glu Lys

370

375

380

Lys Thr Ala Thr Ala Leu Leu Glu Ser Pro Leu Ser Ala Thr Val Glu

385

390

395

400

Asp Ala Leu Gln Ser Phe Leu Lys Ala Glu Glu Leu Gln Pro Gly Phe

405

410

415

Ser Lys Ala Gly Arg Val Tyr Ile Ser Lys Cys Tyr Arg Glu Leu Gly

420

425

430

Lys Asn Ser Glu Ala Arg Trp Trp Met Lys Leu Ala Leu Glu Leu Pro

435

440

445

Asp Val Thr Lys Glu Asp Leu Ala Ile Gln Lys Asp Leu Glu Glu Leu

450

455

460

Glu Val Ile Leu Arg Asp

465

470

<210> 39

<211> 243

<212> PRT

<213> Homo sapiens

<400> 39

Met Glu Gln Gly Ser Gly Arg Leu Glu Asp Phe Pro Val Asn Val Phe

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1 5 10 15
Ser Val Thr Pro Tyr Thr Pro Ser Thr Ala Asp Ile Gln Val Ser Asp
20 25 30
Asp Asp Lys Ala Gly Ala Thr Leu Leu Phe Ser Gly Ile Phe Leu Gly
35 40 45
Leu Val Gly Ile Thr Phe Thr Val Met Gly Trp Ile Lys Tyr Gln Gly
50 55 60
Val Ser His Phe Glu Trp Thr Gln Leu Leu Gly Pro Val Leu Leu Ser
65 70 75 80
Val Gly Val Thr Phe Ile Leu Ile Ala Val Cys Lys Phe Lys Met Leu
85 90 95
Ser Cys Gln Leu Cys Lys Glu Ser Glu Glu Arg Val Pro Asp Ser Glu
100 105 110
Gln Thr Pro Gly Gly Pro Ser Phe Val Phe Thr Gly Ile Asn Gln Pro
115 120 125
Ile Thr Phe His Gly Ala Thr Val Val Gln Tyr Ile Pro Pro Pro Tyr
130 135 140
Gly Ser Pro Glu Pro Met Gly Ile Asn Thr Ser Tyr Leu Gln Ser Val
145 150 155 160
Val Ser Pro Cys Gly Leu Ile Thr Ser Gly Gly Ala Ala Ala Ala Met
165 170 175
Ser Ser Pro Pro Gln Tyr Tyr Thr Ile Tyr Pro Gln Asp Asn Ser Ala
180 185 190
Phe Val Val Asp Glu Gly Cys Leu Ser Phe Thr Asp Gly Gly Asn His
195 200 205

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Arg Pro Asn Pro Asp Val Asp Gln Leu Glu Glu Thr Gln Leu Glu Glu

210

215

220

Glu Ala Cys Ala Cys Phe Ser Pro Pro Pro Tyr Glu Glu Ile Tyr Ser

225

230

235

240

Leu Pro Arg

<210> 40

<211> 270

<212> PRT

<213> Homo sapiens

<400> 40

Met Ala Gly Ala Glu Asp Trp Pro Gly Gln Gln Leu Glu Leu Asp Glu

1

5

10

15

Asp Glu Ala Ser Cys Cys Arg Trp Gly Ala Gln His Ala Gly Ala Arg

20

25

30

Glu Leu Ala Ala Leu Tyr Ser Pro Gly Lys Arg Leu Gln Glu Trp Cys

35

40

45

Ser Val Ile Leu Cys Phe Ser Leu Ile Ala His Asn Leu Val His Leu

50

55

60

Leu Leu Leu Ala Arg Trp Glu Asp Thr Pro Leu Val Ile Leu Gly Val

65

70

75

80

Val Ala Gly Ala Leu Ile Ala Asp Phe Leu Ser Gly Leu Val His Trp

85

90

95

Gly Ala Asp Thr Trp Gly Ser Val Glu Leu Pro Ile Val Gly Lys Ala

100

105

110

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Phe Ile Arg Pro Phe Arg Glu His His Ile Asp Pro Thr Ala Ile Thr

115

120

125

Arg His Asp Phe Ile Glu Thr Asn Gly Asp Asn Cys Leu Val Thr Leu

130

135

140

Leu Pro Leu Leu Asn Met Ala Tyr Lys Phe Arg Thr His Ser Pro Glu

145

150

155

160

Ala Leu Glu Gln Leu Tyr Pro Trp Glu Cys Phe Val Phe Cys Leu Ile

165

170

175

Ile Phe Gly Thr Phe Thr Asn Gln Ile His Lys Trp Ser His Thr Tyr

180

185

190

Phe Gly Leu Pro Arg Trp Val Thr Leu Leu Gln Asp Trp His Val Ile

195

200

205

Leu Pro Arg Lys His His Arg Ile His His Val Ser Pro His Glu Thr

210

215

220

Tyr Phe Cys Ile Thr Thr Gly Trp Leu Asn Tyr Pro Leu Glu Lys Ile

225

230

235

240

Gly Phe Trp Arg Arg Leu Glu Asp Leu Ile Gln Gly Leu Thr Gly Glu

245

250

255

Lys Pro Arg Ala Asp Asp Met Lys Trp Ala Gln Lys Ile Lys

260

265

270

<210> 41

<211> 1131

<212> DNA

<213> Homo sapiens

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<400> 41

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ctcatggcgc tgcctcccat cttcttcggc gccctgcgt ccgtacgtg cgcgcggc 180
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atgccagct gcacactctt ggggtctac ctctttttca aaatattctc ccaggagtac 300
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<210> 42.

<211> 243.

<212> DNA

<213> Homo sapiens

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<400> 42

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ctggtcgcca ccgcgctctg ctgttacctc ttctggctca tcgccatcct ggcgcagctg 180
aacccccctgt tcgggccccca gctgaagaat gagaccatct ggtacgtgcg cttcctgtgg 240
gag 243

<210> 43

<211> 1461

<212> DNA

<213> Homo sapiens

<400> 43

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ggcaccatca ttggtctctg gatcttcgtt tcccccaagt ctgtgctcag caacacggaa 180
gctgtggggc cctgcctcat catatgggcg gcttgccggg tcctcgcgac gctgggtgcc 240
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atcagcctgg cgttttacaa tggactctgg gcctatgatg gatggaatca actcaattac 720
atcacagaag aacttagaaa cccttacaga aacctgcctt tgccattat catcgggatc 780

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cccctggtga cggcgtgcta catcctcatg aacgtgtcct acttcaccgt gatgactgcc 840
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 gtgctgttta tattaagcgg ctttttattt tacttcctgt ttgtccacta caagtttgga 1380
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 ccaccggagg aagaccctga g 1461

<210> 44

<211> 1125

<212> DNA

<213> Homo sapiens

<400> 44

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 gaccttgccg agcactttga ccgaagcgcc caggacactg cgtggatcag cgccctggcc 180
 ctggccgtgc agcaggcagc cagccccgtg ggcagcgccc tgagcacgcg ctggggggcc 240
 cgccccgtgg tgatggttgg gggcgctctc gcctcgtggt gcttcgtctt ctcggtttc 300
 gccagcggtc tgctgcatct ctacctggc ctgggcctcc tcgtggctt tggttgggcc 360
 ctggtgttcg cccccgcct aggcaccctc tcgcgttact tctcccgcg tcgagtcttg 420

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gcggtggggc tggcgctcac cggcaacggg gcctcctcgc tgctcctggc gcccgcttg 480
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cgggctggtg ggcgtcggag gtgtggtgca ggcacaggg ctggtgatga tgctgatgag 1080
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<210> 45

<211> 1050

<212> DNA

<213> Homo sapiens

<400> 45

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tactttgatg tggagcctgc tcaggtcga agcaggctcc tggagtccat gatccctatc 420

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aagatggtca acttccccca gaaaattgca ggtgaactct atggacctct catgctggtc 480
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ggcacccctga tgggcacagc cattggcacc tgcttcggct actggctggg agtctcatcc 600
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<210> 46

<211> 2001

<212> DNA

<213> Homo sapiens

<400> 46

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gctccaagag gggcctggaa gatactggga ctgttctatt atgtgccct ctactacct 480

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ctggctgcct gtgccacggc tggccacaca gctgcacacc tgctcggcag cacgctgtcc 540
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aaggactcca tggccaaggg agctaggccc ggggccagcc gcggcagggc tcgctggggt 1920
ctggcctaca cgctgctgca caaccaacc ctgcaggtct tccgcaagac ggccctgttg 1980

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ggtgccaatg gtgcccagcc c

2001

<210> 47

<211> 1392

<212> DNA

<213> Homo sapiens

<400> 47

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tcgcctttgt ctaacaggtt ccgagtgggt gcccgaaagca tggctgcctt cctttcagtt 1140
caggttccta tggaagatca gatccgtttg aggcctggct ctgaattaca tctgaccccc 1200
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taccaggatc aaatattgca agccacccaa ttataaggc atcctggcca ttgccttcaa 1320
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<210> 48

<211> 1410

<212> DNA

<213> Homo sapiens

<400> 48

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tcaggtgcct ccagtgcctt ggaggtgga ggttcctcag gcttgaggga tgtgtgtccc 720
ctcctgcagc aggccgacga gctgcacagg ggtgatgagc aaggcaagcg ggagggttc 780

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cagctgctgc tcaacaacaa gctgggtgtat ggaagccggc aggactttct ctggcgctg 840
 gcccgagcct acagtgacat gtgtgagctc actgaggagg tgagcgagaa gaagtcatat 900
 gccctagatg gaaaagaaga agcagaggct gctctggaga agggggatga gagtgctgac 960
 tgtcacctgt ggtatgcggt gctttgtggt cagctggctg agcatgagag catccagagg 1020
 cgcattccaga gtggcttttag cttcaaggag catgtggaca aagccattgc tctccagcca 1080
 gaaaacccca tggctcactt tcttcttggc aggtgggtgct atcaggtctc tcacctgagc 1140
 tggctagaaa aaaaaactgc tacagccttg ctgaaagcc ctctcagtgc cactgtggaa 1200
 gatgcctcc agagcttctt aaaggctgaa gaactacagc caggattttc caaagcagga 1260
 agggatatata tttccaagtg ctacagagaa ctagggaaaa actctgaagc tagatgggtg 1320
 atgaagttgg ccttgagct gccagatgtc acgaaggagg atttggtat ccagaaggac 1380
 ctggaagaac tggaagtcatt tttacgagac 1410

<210> 49

<211> 729

<212> DNA

<213> Homo sapiens

<400> 49

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 tacacacca gcaccgtga catccagggt tccgatgatg acaaggcggg ggccaccttg 120
 ctctctcag gcatctttct gggactgggt gggatcacat tcactgtcat gggctggatc 180
 aaataccaag gtgtctccca ctttgaatgg accagctcc ttgggcccgt cctgctgtca 240
 gttgggggtga cattcatcct gattgctgtg tgcaagttca aaatgctctc ctgccagttg 300
 tgcaaagaaa gtgaggaaag ggtcccgac tcggaacaga caccaggagg accatcattt 360
 gttttcactg gcatcaacca accatcacc ttccatgggg cactgtggt gcagtacatc 420
 cctctctctt atggttctcc agagcctatg gggataaata ccagctacct gcagtctgtg 480

98 / 307

gtgagcccct gggcctcat aacctctgga ggggcagcag ccgcatgtc aagtcctcct 540
 caatactaca ccactaccc tcaagataac tctgcatttg tggttgatga gggctgcctt 600
 tctttcacgg acggtggaaa tcacaggccc aatcctgatg ttgaccagct agaagagaca 660
 cagctggaag aggaggcctg tgctgcttc tctcctcccc ctatgaaga aatatactct 720
 ctccctcgc 729

<210> 50

<211> 810

<212> DNA

<213> Homo sapiens

<400> 50

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 tgttgccgct ggggcgcgca gcacgccggg gcccgcgagc tggctgcgct ctactcgcca 120
 ggcaagcgcc tccaggagtg gtgctctgtg atcctgtgct tcagcctcat cgcccacaac 180
 ctgggtccatc tctgtctgct ggcccgttg gaggacacac ccctcgatc actcggtgtt 240
 gttgcagggg ctctcattgc tgacttcttg tctggcctgg tacactgggg tgctgacaca 300
 tggggctctg tggagctgcc cattgtgggg aaggctttca tccgaccctt ccgggagcac 360
 cacattgacc caacagctat cacacggcac gacttcacg agaccaacgg ggacaactgc 420
 ctggtgacac tgctgcoget gctaaacatg gcctacaagt tccgcacca cagccctgaa 480
 gccctggagc agctataccc ctgggagtgc ttcgtcttct gcctgatcat ctccggcacc 540
 ttcaccaacc agatccacaa gtggtcgac acgtactttg ggctgccacg ctgggtcacc 600
 ctctgcagg actggcatgt catcctgcca cgtaaacc atcgcatcca ccacgtctca 660
 ccccacgaga cctacttctg catcaccaca ggctggctca actaccctct ggagaagata 720
 ggcttctggc gacgcctgga ggacctcatc cagggcctga cgggcgagaa gcctcgggca 780
 gatgacatga aatgggcccc gaagatcaaa 810

99 /307

<210> 51

<211> 1551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (98)... (1231)

<400> 51

caaggggaac gtggctttcc ctgcagagcc ggtgtctccg cctgcgtccc tgctgcagca 60

accggagctg gattcggatc ccgaacgcac cctcgcc atg gac tcg gcc ctc agc 115

Met Asp Ser Ala Leu Ser

1 5

gat ccg cat aac ggc agt gcc gag gca ggc ggc ccc acc aac agc act 163

Asp Pro His Asn Gly Ser Ala Glu Ala Gly Gly Pro Thr Asn Ser Thr

10 15 20

acg cgg ccg cct tcc acg ccc gag ggc atc gcg ctg gcc tac ggc agc 211

Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile Ala Leu Ala Tyr Gly Ser

25 30 35

ctc ctg ctc atg gcg ctg ctg ccc atc ttc ttc ggc gcc ctg cgc tcc 259

Leu Leu Leu Met Ala Leu Leu Pro Ile Phe Phe Gly Ala Leu Arg Ser

40 45 50

gta cgc tgc gcc cgc ggc aag aat gct tca gac atg cct gaa aca atc 307

Val Arg Cys Ala Arg Gly Lys Asn Ala Ser Asp Met Pro Glu Thr Ile

55 60 65 70

100/307

acc agc cgg gat gcc gcc cgc ttc ccc atc atc gcc agc tgc aca ctc 355
 Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile Ile Ala Ser Cys Thr Leu
 75 80 85

ttg ggg ctc tac ctc ttt ttc aaa ata ttc tcc cag gag tac atc aac 403
 Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe Ser Gln Glu Tyr Ile Asn
 90 95 100

ctc ctg ctg tcc atg tat ttc ttc gtg ctg gga atc ctg gcc ctg tcc 451
 Leu Leu Leu Ser Met Tyr Phe Phe Val Leu Gly Ile Leu Ala Leu Ser
 105 110 115

cac acc atc agc ccc ttc atg aat aag ttt ttt cca gcc agc ttt cca 499
 His Thr Ile Ser Pro Phe Met Asn Lys Phe Phe Pro Ala Ser Phe Pro
 120 125 130

aat cga cag tac cag ctg ctc ttc aca cag ggt tct ggg gaa aac aag 547
 Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln Gly Ser Gly Glu Asn Lys
 135 140 145 150

gaa gag atc atc aat tat gaa ttt gac acc aag gac ctg gtg tgc ctg 595
 Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr Lys Asp Leu Val Cys Leu
 155 160 165

ggc ctg agc agc atc gtt ggc gtc tgg tac ctg ctg agg aag cac tgg 643
 Gly Leu Ser Ser Ile Val Gly Val Trp Tyr Leu Leu Arg Lys His Trp
 170 175 180

att gcc aac aac ctt ttt ggc ctg gcc ttc tcc ctt aat gga gta gag 691
 Ile Ala Asn Asn Leu Phe Gly Leu Ala Phe Ser Leu Asn Gly Val Glu
 185 190 195

ctc ctg cac ctc aac aat gtc agc act ggc tgc atc ctg ctg ggc gga 739

101/307

Leu Leu His Leu Asn Asn Val Ser Thr Gly Cys Ile Leu Leu Gly Gly
 200 205 210
 ctc ttc atc tac gat gtc ttc tgg gta ttt ggc acc aat gtg atg gtg 787
 Leu Phe Ile Tyr Asp Val Phe Trp Val Phe Gly Thr Asn Val Met Val
 215 220 225 230
 aca gtg gcc aag tcc ttc gag gca cca ata aaa ttg gtg ttt ccc cag 835
 Thr Val Ala Lys Ser Phe Glu Ala Pro Ile Lys Leu Val Phe Pro Gln
 235 240 245
 gat ctg ctg gag aaa ggc ctc gaa gca aac aac ttt gcc atg ctg gga 883
 Asp Leu Leu Glu Lys Gly Leu Glu Ala Asn Asn Phe Ala Met Leu Gly
 250 255 260
 ctt gga gat gtc gtc att cca ggg atc ttc att gcc ttg ctg ctg cgc 931
 Leu Gly Asp Val Val Ile Pro Gly Ile Phe Ile Ala Leu Leu Leu Arg
 265 270 275
 ttt gac atc agc ttg aag aag aat acc cac acc tac ttc tac acc agc 979
 Phe Asp Ile Ser Leu Lys Lys Asn Thr His Thr Tyr Phe Tyr Thr Ser
 280 285 290
 ttt gca gcc tac atc ttc ggc ctg ggc ctt acc atc ttc atc atg cac 1027
 Phe Ala Ala Tyr Ile Phe Gly Leu Gly Leu Thr Ile Phe Ile Met His
 295 300 305 310
 atc ttc aag cat gct cag cct gcc ctc cta tac ctg gtc ccc gcc tgc 1075
 Ile Phe Lys His Ala Gln Pro Ala Leu Leu Tyr Leu Val Pro Ala Cys
 315 320 325
 atc ggt ttt cct gtc ctg gtg gcg ctg gcc aag gga gaa gtg aca gag 1123
 Ile Gly Phe Pro Val Leu Val Ala Leu Ala Lys Gly Glu Val Thr Glu

102/307

330 335 340
atg ttc agt tat gag gag tca aat cct aag gat cca gcg gca gtg aca 1171
Met Phe Ser Tyr Glu Glu Ser Asn Pro Lys Asp Pro Ala Ala Val Thr
345 350 355
gaa tcc aaa gag gga aca gag gca tca gca tcg aag ggg ctg gag aag 1219
Glu Ser Lys Glu Gly Thr Glu Ala Ser Ala Ser Lys Gly Leu Glu Lys
360 365 370
aaa gag aaa tg atgcagctgg tgcccagagcc tctcagggcc agaccagaca 1270
Lys Glu Lys
375
gatgggggct gggcccacac aggcgtgcac cggtagaggg cacaggaggc caagggcagc 1330
tccaggacag ggcagggggc agcaggatac ctccagccag gcctctgtgg cctctgtttc 1390
cttctccctt tcttggccct cctctgtctc tccccacacc ctgcaggcaa aagaaacccc 1450
cagcttcccc cctccccggg agccaggtgg gaaaagtggg tgtgattttt agattttgta 1510
ttgtggactg attttgctc acattaaaaa ctcatcccat g 1551

<210> 52
<211> 1713
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (89)... (334)
<400> 52
tctcagcgcg ctgcccggct ggggaccgc gcacctgcag cgcccgtgc tggccctgc 60

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atcctgcctg ggcatactgc gcccggcc atg acg gcg cac tca ttc gcc etc 112

Met Thr Ala His Ser Phe Ala Leu

1

5

ccg gtc atc atc ttc acc acg ttc tgg gcc etc gtc gcc atc gcc ggg 160

Pro Val Ile Ile Phe Thr Thr Phe Trp Gly Leu Val Gly Ile Ala Gly

10

15

20

ccc tgg ttc gtg ccg aag gga ccc aac cgc gga gtg atc atc acc atg 208

Pro Trp Phe Val Pro Lys Gly Pro Asn Arg Gly Val Ile Ile Thr Met

25

30

35

40

ctg gtc gcc acc gcc gtc tgc tgt tac etc ttc tgg etc atc gcc atc 256

Leu Val Ala Thr Ala Val Cys Cys Tyr Leu Phe Trp Leu Ile Ala Ile

45

50

55

ctg gcg cag ctg aac ccc ctg ttc ggg ccc cag ctg aag aat gag acc 304

Leu Ala Gln Leu Asn Pro Leu Phe Gly Pro Gln Leu Lys Asn Glu Thr

60

65

70

atc tgg tac gtg cgc ttc ctg tgg gag tgaccgcg gcccccagacc 350

Ile Trp Tyr Val Arg Phe Leu Trp Glu

75

80

caggtgccca gctctcgga tgaactgtgc tccactgtcc ctgacaaccc ctctgtccgg 410

accctccccc acacaactat gtctgggtcac cagctccctc ctgttggtcac ccagagaccc 470

ggacccgcag ggctgcctg gttcctggaa gtcttcccag tcttcccagc cagcccgggc 530

cctgggggagc cctgggcaca gcagcggccg aggggatgtc ctgtccaat accgcactg 590

ctctggagtt tgccctcttt cccaaggaga tgctgtggg gagctggtat ggggtggggtc 650

tttcccttta cagacggggc agatgccagg actcagccca tctgaggag gacacgtgtc 710

ctcatggaga ggggtgtccg gcccgagcgg gggagtcagt gccagtcag cagctctgcc 770

104/307

accatcctgc tgggaactgg gggggcctct attgggttat aggcaaggcc tttctcttg 830
catggaattg ttaatcttct gacacgtcta gatgtgaaat ttctgaaaat gttgaagcag 890
agaacattc acacacaaaa agcaacatag tcatgtgggt ccagatggcc tcagtcctag 950
atgttggcac cctttgctgt gtctcctcag agtatcctgt tccgcctcct gccacctgga 1010
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caggggtccc ggacctctcc agccttggcc tcacgcttac ccgagctccc agtgtggta 1370
gcacagagct caccacactt gcctggctcc cagctggggc ctgtcctcac tgggtctcca 1430
ggggaagaaa cgacagctc acttctgtat ggactgctga tgtggcctgc catcctgttc 1490
agcgggcatt gtctttggag cagcaggaga ataggatgcc tctcactcac atgccagttc 1550
ctggctggcc agctgctcag ggctcaggt ggggcctccc attgacatcc tccccctaca 1610
ctcctctct gagectccgt cggcctcct gttgggtaag ggtgttgagt gtgacttggt 1670
ctgaaaacct gttcatata taataataa tggatgaa aag 1713

<210> 53

<211> 1758

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (190)... (1653)

<400> 53

105/307

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 gcagggtcac ggaggaagcc agctccccta gtccaggccg agcttgcaact tgcgtcttgt 120
 ctgctgctgc tgaaccaaga tttagctgtg cgccctcctt gcagtctcct ggaaccagca 180
 ggaggaaac atg ggg gat act ggc ctg aga aag cgg aga gag gat gag 228

Met Gly Asp Thr Gly Leu Arg Lys Arg Arg Glu Asp Glu

1

5

10

aag tcg atc cag agc caa gag cct aag acc acc agt ctc caa aag gag 276

Lys Ser Ile Gln Ser Gln Glu Pro Lys Thr Thr Ser Leu Gln Lys Glu

15

20

25

ctg ggc ctc atc agt ggc atc tcc atc atc gtg ggc acc atc att ggc 324

Leu Gly Leu Ile Ser Gly Ile Ser Ile Ile Val Gly Thr Ile Ile Gly

30

35

40

45

tct ggg atc ttc gtt tcc ccc aag tct gtg ctc agc aac acg gaa gct 372

Ser Gly Ile Phe Val Ser Pro Lys Ser Val Leu Ser Asn Thr Glu Ala

50

55

60

gtg ggg ccc tgc ctc atc ata tgg gcg gct tgc ggg gtc ctc gcg acg 420

Val Gly Pro Cys Leu Ile Ile Trp Ala Ala Cys Gly Val Leu Ala Thr

65

70

75

ctg ggt gcc ctg tgc ttt gcg gag ctt ggc aca atg atc acc aag tca 468

Leu Gly Ala Leu Cys Phe Ala Glu Leu Gly Thr Met Ile Thr Lys Ser

80

85

90

ggg gga gag tat ccc tac ctg atg gag gcc tac ggg ccc atc ccc gcc 516

Gly Gly Glu Tyr Pro Tyr Leu Met Glu Ala Tyr Gly Pro Ile Pro Ala

95

100

105

tac ctc ttc tcc tgg gcc agc ctg atc gtc att aag ccc acg tcc ttc 564

106/307

Tyr Leu Phe Ser Trp Ala Ser Leu Ile Val Ile Lys Pro Thr Ser Phe
 110 115 120 125
 gcc atc atc tgc ctc agc ttc tcc gag tat gtg tgt gcg ccc ttc tat. 612
 Ala Ile Ile Cys Leu Ser Phe Ser Glu Tyr Val Cys Ala Pro Phe Tyr
 130 135 140
 gtg ggc tgc aag cct cct caa atc gtt gtg aaa tgc ctg gcc gcc gcc 660
 Val Gly Cys Lys Pro Pro Gln Ile Val Val Lys Cys Leu Ala Ala Ala
 145 150 155
 gcc atc ttg ttc atc tcg aca gtg aac tca ctg agc gtg cgg ctg gga 708
 Ala Ile Leu Phe Ile Ser Thr Val Asn Ser Leu Ser Val Arg Leu Gly
 160 165 170
 agc tac gtc cag aac atc ttc acc gcg gcc aag ctg gtg atc gtg gcc. 756
 Ser Tyr Val Gln Asn Ile Phe Thr Ala Ala Lys Leu Val Ile Val Ala.
 175 180 185
 atc atc atc atc agc ggg ctg gtg ctc ctg gcc caa gga aac aca aag 804
 Ile Ile Ile Ile Ser Gly Leu Val Leu Leu Ala Gln Gly Asn Thr Lys
 190 195 200 205
 aat ttt gat aat tct ttc gag ggc gcc cag ctg tct gtg gga gcc atc 852
 Asn Phe Asp Asn Ser Phe Glu Gly Ala Gln Leu Ser Val Gly Ala Ile
 210 215 220
 agc ctg gcg ttt tac aat gga ctc tgg gcc tat gat gga tgg aat caa 900
 Ser Leu Ala Phe Tyr Asn Gly Leu Trp Ala Tyr Asp Gly Trp Asn Gln
 225 230 235
 ctc aat tac atc aca gaa gaa ctt aga aac cct tac aga aac ctg cct 948
 Leu Asn Tyr Ile Thr Glu Glu Leu Arg Asn Pro Tyr Arg Asn Leu Pro

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240	245	250	
ttg gcc att atc atc ggg atc ccc ctg gtg acg gcg tgc tac atc ctc			996
Leu Ala Ile Ile Ile Gly Ile Pro Leu Val Thr Ala Cys Tyr Ile Leu			
255	260	265	
atg aac gtg tcc tac ttc acc gtg atg act gcc acc gaa ctc ctg cag			1044
Met Asn Val Ser Tyr Phe Thr Val Met Thr Ala Thr Glu Leu Leu Gln			
270	275	280	285
tcc cag gcg gtg gct gtg aca ttt ggt gac cgt gtt ctc tat cct gct			1092
Ser Gln Ala Val Ala Val Thr Phe Gly Asp Arg Val Leu Tyr Pro Ala			
290	295	300	
tct tgg atc gtt cca ctt ttt gtg gca ttt tca acc atc ggt gct gct			1140
Ser Trp Ile Val Pro Leu Phe Val Ala Phe Ser Thr Ile Gly Ala Ala			
305	310	315	
aac ggg acc tgc ttc aca gcg ggc aga ctc att tac gtg gcg ggc cgg			1188
Asn Gly Thr Cys Phe Thr Ala Gly Arg Leu Ile Tyr Val Ala Gly Arg			
320	325	330	
gag ggt cac atg ctc aaa gtg ctt tct tac atc agc gtc agg cgc ctc			1236
Glu Gly His Met Leu Lys Val Leu Ser Tyr Ile Ser Val Arg Arg Leu			
335	340	345	
act cca gcc ccc gcc atc atc ttt tat ggt atc ata gca acg att tat			1284
Thr Pro Ala Pro Ala Ile Ile Phe Tyr Gly Ile Ile Ala Thr Ile Tyr			
350	355	360	365
atc atc cct ggt gac ata aac tcg tta gtc aat tat ttc agc ttt gcc			1332
Ile Ile Pro Gly Asp Ile Asn Ser Leu Val Asn Tyr Phe Ser Phe Ala			
370	375	380	

108/307

gca tgg ctg ttt tat ggc ctg acg att cta gga ctc atc gtg atg aga 1380
Ala Trp Leu Phe Tyr Gly Leu Thr Ile Leu Gly Leu Ile Val Met Arg
385 390 395
ttt aca agg aaa gag ctg gaa agg cct atc aag gtg ccc gta gtc att 1428
Phe Thr Arg Lys Glu Leu Glu Arg Pro Ile Lys Val Pro Val Val Ile
400 405 410
ccc gtc ttg atg aca ctc atc tct gtg ttt ttg gtt ctg gct cca atc 1476
Pro Val Leu Met Thr Leu Ile Ser Val Phe Leu Val Leu Ala Pro Ile
415 420 425
atc agc aag ccc acc tgg gag tac ctc tac tgt gtg ctg ttt ata tta 1524
Ile Ser Lys Pro Thr Trp Glu Tyr Leu Tyr Cys Val Leu Phe Ile Leu
430 435 440 445
agc ggc ctt tta ttt tac ttc ctg ttt gtc cac tac aag ttt gga tgg 1572
Ser Gly Leu Leu Phe Tyr Phe Leu Phe Val His Tyr Lys Phe Gly Trp
450 455 460
gct cag aaa atc tca aag ccg att acc atg cac ctt cag atg cta atg 1620
Ala Gln Lys Ile Ser Lys Pro Ile Thr Met His Leu Gln Met Leu Met
465 470 475
gaa gtg gtc cca ccg gag gaa gac cct gag taacaagctc cgtctcttgt 1670
Glu Val Val Pro Pro Glu Glu Asp Pro Glu
480 485
agccaagtca gctgaattta ttttcttaag caatatttgt gggtatttct tctttttttt 1730
cttacgaata aaatatactc agatgttt 1758
<210> 54

109/307

<211> 1550

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (154)... (1281)

<400> 54

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gggcctccgc ccgcctggga agcagagaga aagccgggcc cagcccttcc tcacccttcc 120

cctccccgca ccgccggag aggtcggacg gcg atg acc ccc cag ccc gcc gga 174

Met Thr Pro Gln Pro Ala Gly

1

5

ccc ccg gat ggg ggc tgg ggc tgg gtg gtg gcg gcc gca gcc ttc gcg 222

Pro Pro Asp Gly Gly Trp Gly Trp Val Val Ala Ala Ala Ala Phe Ala

10

15

20

ata aac ggg ctg tcc tac ggg ctg ctg cgc tcg ctg ggc ctt gcc ttc 270

Ile Asn Gly Leu Ser Tyr Gly Leu Leu Arg Ser Leu Gly Leu Ala Phe

25

30

35

cct gac ctt gcc gag cac ttt gac cga agc gcc cag gac act gcg tgg 318

Pro Asp Leu Ala Glu His Phe Asp Arg Ser Ala Gln Asp Thr Ala Trp

40

45

50

55

atc agc gcc ctg gcc ctg gcc gtg cag cag gca gcc agc ccc gtg ggc 366

Ile Ser Ala Leu Ala Leu Ala Val Gln Gln Ala Ala Ser Pro Val Gly

60

65

70

agc gcc ctg agc acg cgc tgg ggg gcc cgc ccc gtg gtg atg gtt ggg 414

110/307

Ser Ala Leu Ser Thr Arg Trp Gly Ala Arg Pro Val Val Met Val Gly
 75 80 85
 ggc gtc ctc gcc tcg ctg ggc ttc gtc ttc tcg gct ttc gcc agc ggt 462
 Gly Val Leu Ala Ser Leu Gly Phe Val Phe Ser Ala Phe Ala Ser Gly
 90 95 100
 ctg ctg cat ctc tac ctc ggc ctg ggc ctc ctc gct ggc ttt ggt tgg 510
 Leu Leu His Leu Tyr Leu Gly Leu Gly Leu Leu Ala Gly Phe Gly Trp
 105 110 115
 gcc ctg gtg ttc gcc ccc gcc cta ggc acc ctc tcg cgt tac ttc tcc 558
 Ala Leu Val Phe Ala Pro Ala Leu Gly Thr Leu Ser Arg Tyr Phe Ser
 120 125 130 135
 cgc cgt cga gtc ttg gcg gtg ggg ctg gcg ctc acc ggc aac ggg gcc 606
 Arg Arg Arg Val Leu Ala Val Gly Leu Ala Leu Thr Gly Asn Gly Ala
 140 145 150
 tcc tcg ctg ctc ctg gcg ccc gcc ttg cag ctt ctc ctc gat act ttc 654
 Ser Ser Leu Leu Leu Ala Pro Ala Leu Gln Leu Leu Leu Asp Thr Phe
 155 160 165
 ggc tgg cgg ggc gct ctg ctc ctc ctc ggc gcg atc acc ctc cac ctc 702
 Gly Trp Arg Gly Ala Leu Leu Leu Leu Gly Ala Ile Thr Leu His Leu
 170 175 180
 acc ccc tgt ggc gcc ctg ctg cta ccc ctg gtc ctt cct gga gac ccc 750
 Thr Pro Cys Gly Ala Leu Leu Leu Pro Leu Val Leu Pro Gly Asp Pro
 185 190 195
 cca gcc cca ccg cgt agt ccc cta gct gcc ctc ggc ctg agt ctg ttc 798
 Pro Ala Pro Pro Arg Ser Pro Leu Ala Ala Leu Gly Leu Ser Leu Phe

111/307

200 205 210 215
 aca cgc cgg gcc ttc tca atc ttt gct cta ggc aca gcc ctg gtt ggg 846
 Thr Arg Arg Ala Phe Ser Ile Phe Ala Leu Gly Thr Ala Leu Val Gly
 220 225 230
 ggc ggg tac ttc gtt cct tac gtg cac ttg gct ccc cgc ttt aga ccg 894
 Gly Gly Tyr Phe Val Pro Tyr Val His Leu Ala Pro Arg Phe Arg Pro
 235 240 245
 ggg cct ggg ggg ata cgg agc agc gct ggt ggt ggc cgt ggc tgc gat 942
 Gly Pro Gly Gly Ile Arg Ser Ser Ala Gly Gly Gly Arg Gly Cys Asp
 250 255 260
 ggg gga tgc ggg cgc ccg gct ggt ctg cgg gtg gct ggc aga cca agg 990
 Gly Gly Cys Gly Arg Pro Ala Gly Leu Arg Val Ala Gly Arg Pro Arg
 265 270 275
 ctg ggt gcc cct ccc gcg gct gct ggc cgt att cgg ggc tct gac tgg 1038
 Leu Gly Ala Pro Pro Ala Ala Ala Gly Arg Ile Arg Gly Ser Asp Trp
 280 285 290 295
 gct ggg gct gtg ggt ggt ggg gct ggt gcc cgt ggt ggg cgg cga aga 1086
 Ala Gly Ala Val Gly Gly Gly Ala Gly Ala Arg Gly Gly Arg Arg Arg
 300 305 310
 gag ctg ggg ggg tcc cct gct ggc cgc ggc tgt ggc cta tgg gct gag 1134
 Glu Leu Gly Gly Ser Pro Ala Gly Arg Gly Cys Gly Leu Trp Ala Glu
 315 320 325
 cgc ggg gag tta cgc ccc gct ggt ttt cgg tgt act ccc cgg gct ggt 1182
 Arg Gly Glu Leu Arg Pro Ala Gly Phe Arg Cys Thr Pro Arg Ala Gly
 330 335 340

112/307

ggg cgt cgg agg tgt ggt gca ggc cac agg gct ggt gat gat gct gat ... 1230
Gly Arg Arg Arg Cys Gly Ala Gly His Arg Ala Gly Asp Asp Ala Asp
345 350 355
gag cct cgg ggg gct cct ggg ccc tcc cct gtc agg ctt cct aag gga 1278
Glu Pro Arg Gly Ala Pro Gly Pro Ser Pro Val Arg Leu Pro Lys Gly
360 365 370 375
tg agacaggaga cttcacgcc tctttctctc tgtctggttc tttgatactc 1330
tccggcagct tcattacat agggttgccc agggcgctgc cctcctgttg tccagcctcc 1390
cctccagcca cgcctcccc agagacgggg gagctgcttc ccgtcccca ggcagtcttg 1450
ctgtccccag gaggccttg ctcactctg gacaccactt gttgattatt ttctgtttg 1510
agccccctcc ccaataaaga atttttatcg gggtttcctg 1550

<210> 55

<211> 1485

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (101)... (1153)

<400> 55

ctctcctcga ccctggacgt ctaccttcg gagggccaca tcttggccac tccgcgcgcg 60
gggctagcgc gggtttcagc gacgggagcc ctcaaggagc atg gca act aca ggc 115
Met Ala Thr Thr Ala
1 5
gcg ccg gcg ggc ggc gcc cga aat gga gct ggc ccg gaa tgg gga ggg 163

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Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly Pro Glu Trp Gly Gly
 10 15 20
 ttc gaa gaa aac atc cag ggc gga ggc tca gct gtg att gac atg gag 211
 Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala Val Ile Asp Met Glu
 25 30 35
 aac atg gat gat acc tca ggc tct agc ttc gag gat atg ggt gag ctg 259
 Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu Asp Met Gly Glu Leu
 40 45 50
 cat cag cgc ctg cgc gag gaa gaa gta gac gct gat gca gct gat gca 307
 His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala Asp Ala Ala Asp Ala
 55 60 65
 gct gct gct gaa gag gag gat gga gag ttc ctg ggc atg aag ggc ttt 355
 Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu Gly Met Lys Gly Phe
 70 75 80 85
 aag gga cag ctg agc cgg cag gtg gca gat cag atg tgg cag gct ggg 403
 Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln Met Trp Gln Ala Gly
 90 95 100
 aaa aga caa gcc tcc agg gcc ttc agc ttg tac gcc aac atc gac atc 451
 Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr Ala Asn Ile Asp Ile
 105 110 115
 ctc aga ccc tac ttt gat gtg gag cct gct cag gtg cga agc agg ctc 499
 Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln Val Arg Ser Arg Leu
 120 125 130
 ctg gag tcc atg atc cct atc aag atg gtc aac ttc ccc cag aaa att 547
 Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn Phe Pro Gln Lys Ile

114/307

135 140 145
gca ggt gaa ctc tat gga cct ctc atg ctg gtc ttc act ctg gtt gct 595
Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val Phe Thr Leu Val Ala
150 155 160 165
atc cta ctc cat ggg atg aag acg tct gac act att atc cgg gag ggc 643
Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr Ile Ile Arg Glu Gly
170 175 180
acc ctg atg ggc aca gcc att ggc acc tgc ttc ggc tac tgg ctg gga 691
Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe Gly Tyr Trp Leu Gly
185 190 195
gtc tca tcc ttc att tac ttc ctt gcc tac ctg tgc aac gcc cag atc 739
Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu Cys Asn Ala Gln Ile
200 205 210
acc atg ctg cag atg ttg gca ctg ctg ggc tat ggc ctc ttt ggg cat 787
Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr Gly Leu Phe Gly His
215 220 225
tgc att gtc ctg ttc atc acc tat aat atc cac ctc cac gcc ctc ttc 835
Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His Leu His Ala Leu Phe
230 235 240 245
tac ctc ttc tgg ctg ttg gtg ggt gga ctg tcc aca ctg cgc atg gta 883
Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser Thr Leu Arg Met Val
250 255 260
gca gtg ttg gtg tct cgg acc gtg ggc ccc aca cag cgg ctg ctc ctc 931
Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr Gln Arg Leu Leu Leu
265 270 275

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tgt ggc acc ctg gct gcc cta cac atg ctc ttc ctg ctc tat ctg cat 979
 Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe Leu Leu Tyr Leu His
 280 285 290
 ttt gcc tac cac aaa gtg gta gag ggg atc ctg gac aca ctg gag ggc 1027
 Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu Asp Thr Leu Glu Gly
 295 300 305
 ccc aac atc ccg ccc atc cag agg gtc ccc aga gac atc cct gcc atg 1075
 Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg Asp Ile Pro Ala Met
 310 315 320 325
 ctc cct gct gct cgg ctt ccc acc acc gtc ctc aac gcc aca gcc aaa 1123
 Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu Asn Ala Thr Ala Lys
 330 335 340
 gct gtt gcg gtg acc ctg cag tca cac tgacccacc tgaaattctt 1170
 Ala Val Ala Val Thr Leu Gln Ser His
 345 350
 ggccagtcct ctttcccgca gctgcagaga ggaggaagac tattaaagga cagtcctgat 1230
 gacatgtttc gtagatgggg tttgcagctg ccactgagct gtagctgcgt aagtacctcc 1290
 ttgatgcctg tcggcacttc tgaaaggcac aaggccaaga actcctggcc aggactgcaa 1350
 ggctctgcag ccaatgcaga aaatgggtca gtcctttga gaaccctcc ccacctaccc 1410
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 gttgattgaa gtctg 1485

<210> 56

<211> 2694

<212> DNA

116/307

<213> Homo sapiens

<220>

<221> CDS

<222> (80)... (2083)

<400> 56

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gcaggagaag ggccagaga atg tgc tcc cag cca gca ggg aac cag acc tcc 112

Met Ser Ser Gln Pro Ala Gly Asn Gln Thr Ser

1

5

10

ccc ggg gcc aca gag gac tac tcc tat ggc agc tgg tac atc gat gag 160

Pro Gly Ala Thr Glu Asp Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu

15

20

25

ccc cag ggg ggc gag gag ctc cag cca gag ggg gaa gtg ccc tcc tgc 208

Pro Gln Gly Gly Glu Glu Leu Gln Pro Glu Gly Glu Val Pro Ser Cys

30

35

40

cac acc agc ata cca ccc ggc ctg tac cac gcc tgc ctg gcc tgc ctg 256

His Thr Ser Ile Pro Pro Gly Leu Tyr His Ala Cys Leu Ala Ser Leu

45

50

55

tca atc ctt gtg ctg ctg ctc ctg gcc atg ctg gtg agg cgc cgc cag 304

Ser Ile Leu Val Leu Leu Leu Leu Ala Met Leu Val Arg Arg Arg Gln

60

65

70

75

ctc tgg cct gac tgt gtg cgt ggc agg ccc ggc ctg ccc agc cct gtg 352

Leu Trp Pro Asp Cys Val Arg Gly Arg Pro Gly Leu Pro Ser Pro Val

80

85

90

gat ttc ttg gct ggg gac agg ccc cgg gca gtg cct gct gct gtt ttc 400

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Asp Phe Leu Ala Gly Asp Arg Pro Arg Ala Val Pro Ala Ala Val Phe
 95 100 105
 atg gtc ctc ttg agc tcc ctg tgt ttg ctg ctc ccc gac gag gac gca 448
 Met Val Leu Leu Ser Ser Leu Cys Leu Leu Leu Pro Asp Glu Asp Ala
 110 115 120
 ttg ccc ttc ctg act ctc gcc tca gca ccc agc caa gat ggg aaa act 496
 Leu Pro Phe Leu Thr Leu Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr
 125 130 135
 gag gct cca aga ggg gcc tgg aag ata ctg gga ctg ttc tat tat gct 544
 Glu Ala Pro Arg Gly Ala Trp Lys Ile Leu Gly Leu Phe Tyr Tyr Ala
 140 145 150 155
 gcc ctc tac tac cct ctg gct gcc tgt gcc acg gct ggc cac aca gct 592
 Ala Leu Tyr Tyr Pro Leu Ala Ala Cys Ala Thr Ala Gly His Thr Ala
 160 165 170
 gca cac ctg ctc ggc agc acg ctg tcc tgg gcc cac ctt ggg gtc cag 640
 Ala His Leu Leu Gly Ser Thr Leu Ser Trp Ala His Leu Gly Val Gln
 175 180 185
 gtc tgg cag agg gca gag tgt ccc cag gtg ccc aag atc tac aag tac 688
 Val Trp Gln Arg Ala Glu Cys Pro Gln Val Pro Lys Ile Tyr Lys Tyr
 190 195 200
 tac tcc ctg ctg gcc tcc ctg cct ctc ctg ctg ggc ctc gga ttc ctg 736
 Tyr Ser Leu Leu Ala Ser Leu Pro Leu Leu Leu Gly Leu Gly Phe Leu
 205 210 215
 agc ctt tgg tac cct gtg cag ctg gtg aga agc ttc agc cgt agg aca 784
 Ser Leu Trp Tyr Pro Val Gln Leu Val Arg Ser Phe Ser Arg Arg Thr

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220 225 230 235
gga gca ggc tcc aag ggg ctg cag agc agc tac tct gag gaa tat ctg 832
Gly Ala Gly Ser Lys Gly Leu Gln Ser Ser Tyr Ser Glu Glu Tyr Leu
240 245 250
agg aac ctc ctt tgc agg aag aag ctg gga agc agc tac cac acc tcc 880
Arg Asn Leu Leu Cys Arg Lys Lys Leu Gly Ser Ser Tyr His Thr Ser
255 260 265
aag cat ggc ttc ctg tcc tgg gcc cgc gtc tgc ttg aga cac tgc atc 928
Lys His Gly Phe Leu Ser Trp Ala Arg Val Cys Leu Arg His Cys Ile
270 275 280
tac act cca cag cca gga ttc cat ctc ccg ctg aag ctg gtg ctt tca 976
Tyr Thr Pro Gln Pro Gly Phe His Leu Pro Leu Lys Leu Val Leu Ser
285 290 295
gct aca ctg aca ggg acg gcc att tac cag gtg gcc ctg ctg ctg ctg 1024
Ala Thr Leu Thr Gly Thr Ala Ile Tyr Gln Val Ala Leu Leu Leu Leu
300 305 310 315
gtg ggc gtg gta ccc act atc cag aag gtg agg gca ggg gtc acc acg 1072
Val Gly Val Val Pro Thr Ile Gln Lys Val Arg Ala Gly Val Thr Thr
320 325 330
gat gtc tcc tac ctg ctg gcc ggc ttt gga atc gtg ctc tcc gag gac 1120
Asp Val Ser Tyr Leu Leu Ala Gly Phe Gly Ile Val Leu Ser Glu Asp
335 340 345
aag cag gag gtg gtg gag ctg gtg aag cac cat ctg tgg gct ctg gaa 1168
Lys Gln Glu Val Val Glu Leu Val Lys His His Leu Trp Ala Leu Glu
350 355 360

119/307

gtg tgc tac atc tca gcc ttg gtc ttg tcc tgc tta ctc acc ttc ctg	1216
Val Cys Tyr Ile Ser Ala Leu Val Leu Ser Cys Leu Leu Thr Phe Leu	
365 370 375	
gtc ctg atg cgc tca ctg gtg aca cac agg acc aac ctt cga gct ctg	1264
Val Leu Met Arg Ser Leu Val Thr His Arg Thr Asn Leu Arg Ala Leu	
380 385 390 395	
cac cga gga gct gcc ctg gac ttg agt ccc ttg cat cgg agt ccc cat	1312
His Arg Gly Ala Ala Leu Asp Leu Ser Pro Leu His Arg Ser Pro His	
400 405 410	
ccc tcc cgc caa gcc ata ttc tgt tgg atg agc ttc agt gcc tac cag	1360
Pro Ser Arg Gln Ala Ile Phe Cys Trp Met Ser Phe Ser Ala Tyr Gln	
415 420 425	
aca gcc ttt atc tgc ctt ggg ctc ctg gtg cag cag atc atc ttc ttc	1408
Thr Ala Phe Ile Cys Leu Gly Leu Leu Val Gln Gln Ile Ile Phe Phe	
430 435 440	
ctg gga acc acg gcc ctg gcc ttc ctg gtg ctc atg cct gtg ctc cat	1456
Leu Gly Thr Thr Ala Leu Ala Phe Leu Val Leu Met Pro Val Leu His	
445 450 455	
ggc agg aac ctc ctg ctc ttc cgt tcc ctg gag tcc tcg tgg ccc ttc	1504
Gly Arg Asn Leu Leu Leu Phe Arg Ser Leu Glu Ser Ser Trp Pro Phe	
460 465 470 475	
tgg ctg act ttg gcc ctg gct gtg atc ctg cag aac atg gca gcc cat	1552
Trp Leu Thr Leu Ala Leu Ala Val Ile Leu Gln Asn Met Ala Ala His	
480 485 490	
tgg gtc ttc ctg gag act cat gat gga cac cca cag ctg acc aac cgg	1600

120/307

Trp Val Phe Leu Glu Thr His Asp Gly His Pro Gln Leu Thr Asn Arg
 495 500 505
 cga gtg ctc tat gca gcc acc ttt ctt ctc ttc ccc ctc aat gtg ctg 1648
 Arg Val Leu Tyr Ala Ala Thr Phe Leu Leu Phe Pro Leu Asn Val Leu
 510 515 520
 gtg ggt gcc atg gtg gcc acc tgg cga gtg ctc ctc tct gcc ctc tac 1696
 Val Gly Ala Met Val Ala Thr Trp Arg Val Leu Leu Ser Ala Leu Tyr
 525 530 535
 aac gcc atc cac ctt ggc cag atg gac ctc agc ctg ctg cca ccg aga 1744
 Asn Ala Ile His Leu Gly Gln Met Asp Leu Ser Leu Leu Pro Pro Arg
 540 545 550 555
 gcc gcc act ctc gac ccc ggc tac tac acg tac cga aac ttc ttg aag 1792
 Ala Ala Thr Leu Asp Pro Gly Tyr Tyr Thr Tyr Arg Asn Phe Leu Lys
 560 565 570
 att gaa gtc agc cag tcg cat cca gcc atg aca gcc ttc tgc tcc ctg 1840
 Ile Glu Val Ser Gln Ser His Pro Ala Met Thr Ala Phe Cys Ser Leu
 575 580 585
 ctc ctg caa gcg cag agc ctc cta ccc agg acc atg gca gcc ccc cag 1888
 Leu Leu Gln Ala Gln Ser Leu Leu Pro Arg Thr Met Ala Ala Pro Gln
 590 595 600
 gac agc ctc aga cca ggg gag gaa gac gaa ggg atg cag ctg cta cag 1936
 Asp Ser Leu Arg Pro Gly Glu Glu Asp Glu Gly Met Gln Leu Leu Gln
 605 610 615
 aca aag gac tcc atg gcc aag gga gct agg ccc ggg gcc agc cgc ggc 1984
 Thr Lys Asp Ser Met Ala Lys Gly Ala Arg Pro Gly Ala Ser Arg Gly

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620	625	630	635	
agg gct cgc tgg ggt ctg gcc tac acg ctg ctg cac aac cca acc ctg				2032
Arg Ala Arg Trp Gly Leu Ala Tyr Thr Leu Leu His Asn Pro Thr Leu				
	640	645	650	
cag gtc ttc cgc aag acg gcc ctg ttg ggt gcc aat ggt gcc cag ccc				2080
Gln Val Phe Arg Lys Thr Ala Leu Leu Gly Ala Asn Gly Ala Gln Pro				
	655	660	665	
tgagggcagg gaaggtcaac ccacctgccc atctgtgctg aggcattgtc				2130
ctgcctacca tctcctccc tccccggctc tctcccagc atcacaccag ccatgcagcc				2190
agcaggtcct ccggatcacc gtggttgggt ggaggtctgt ctgcactggg agcctcagga				2250
gggtcttctc caccacctt ggctatggga gagccagcag gggttctgga gaaagaaact				2310
ggtggggttag ggccttggtc caggagccag ttgagccagg gcagccacat ccaggcgtct				2370
ccctaccctg gctctgccat cagccttgaa gggcctcgat gaagccttct ctggaaccac				2430
tccagcccag ctccacctca gccttggcct tcacgtgtg gaagcagcca aggcacttcc				2490
tcacccctc agcgcacagg acctctctgg ggagtggccg gaaagctccc gggcctctgg				2550
cctgcagggc agcccaagtc atgactcaga ccaggtccca cactgagctg cccacactcg				2610
agagccagat atttttgtag tttttatgcc tttggtatt atgaaagagg ttagtgtgtt				2670
ccctgaata aacttgttcc tgag				2694

<210> 57

<211> 3297

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

122/307

<222> (83)... (1477)

<400> 57

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tccccaccca gaaaccgcga gc atg att gtc tgc ctc ctt ttc atg atg att      112
      Met Ile Val Cys Leu Leu Phe Met Met Ile
      1           5           10
tta ttg gca aag gaa gtt caa ctg gta gac caa aca gat tca cct tta      160
Leu Leu Ala Lys Glu Val Gln Leu Val Asp Gln Thr Asp Ser Pro Leu
      15           20           25
ctt agt ctc ctt gga cag aca agc tca ctt tca tgg cat ctt gtg gat      208
Leu Ser Leu Leu Gly Gln Thr Ser Ser Leu Ser Trp His Leu Val Asp
      30           35           40
att gtg tgc tac cag agt gtg cta agt tat ttc agc agc cat tac ccg      256
Ile Val Ser Tyr Gln Ser Val Leu Ser Tyr Phe Ser Ser His Tyr Pro
      45           50           55
ccg tcc atc atc ctg gca aaa gaa tct tat gct gaa tta atc atg aag      304
Pro Ser Ile Ile Leu Ala Lys Glu Ser Tyr Ala Glu Leu Ile Met Lys
      60           65           70
ctc cta aaa gtg tct gcg ggc ctt tct att cct act gac agc cag aag      352
Leu Leu Lys Val Ser Ala Gly Leu Ser Ile Pro Thr Asp Ser Gln Lys
      75           80           85           90
cat ctt gat gca gtt cca aaa tgc caa gct ttt act cat cag atg gtt      400
His Leu Asp Ala Val Pro Lys Cys Gln Ala Phe Thr His Gln Met Val
      95           100           105
caa ttc ctc agc acc ctg gaa caa aat gga aaa atc acc tta gca gtc      448

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Gln Phe Leu Ser Thr Leu Glu Gln Asn Gly Lys Ile Thr Leu Ala Val
 110 115 120
 cta gaa cag gaa atg tct aag ctc tta gac gat atc att gtc ttt aac 496
 Leu Glu Gln Glu Met Ser Lys Leu Leu Asp Asp Ile Ile Val Phe Asn
 125 130 135
 ccg ccc gac atg gac agc cag acc cgc cac atg gcc ctc agc agc ctc 544
 Pro Pro Asp Met Asp Ser Gln Thr Arg His Met Ala Leu Ser Ser Leu
 140 145 150
 ttt atg gaa gtc ctg atg atg atg aac aac gcg act att cca aca gca 592
 Phe Met Glu Val Leu Met Met Met Asn Asn Ala Thr Ile Pro Thr Ala
 155 160 165 170
 gag ttc ctt cgg ggc agt atc cgg acc tgg att ggc caa aaa atg cat 640
 Glu Phe Leu Arg Gly Ser Ile Arg Thr Trp Ile Gly Gln Lys Met His
 175 180 185
 ggg ctg gtg gtg ctg ccc ctt tta aca gca gcc tgc cag agc ctg gcg 688
 Gly Leu Val Val Leu Pro Leu Leu Thr Ala Ala Cys Gln Ser Leu Ala
 190 195 200
 tcc gtc cgc cac atg gct gag act aca gaa gcc tgc atc act gcc tac 736
 Ser Val Arg His Met Ala Glu Thr Thr Glu Ala Cys Ile Thr Ala Tyr
 205 210 215
 ttc aaa gaa agc cct ctc aat cag aat tca gga tgg gga ccc att ctg 784
 Phe Lys Glu Ser Pro Leu Asn Gln Asn Ser Gly Trp Gly Pro Ile Leu
 220 225 230
 gta tcc ctt cag gtt ccc gag ctc acc atg gaa gag ttc ctg cag gag 832
 Val Ser Leu Gln Val Pro Glu Leu Thr Met Glu Glu Phe Leu Gln Glu

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235 240 245 250
tgc ctc acc ttg ggc agt tac ttg act ctt tac gtc tac ttg ctt cag 880
Cys Leu Thr Leu Gly Ser Tyr Leu Thr Leu Tyr Val Tyr Leu Leu Gln
 255 260 265
tgt tta aac agc gaa cag act tta agg aat gaa atg aaa gtg ctg ctc 928
Cys Leu Asn Ser Glu Gln Thr Leu Arg Asn Glu Met Lys Val Leu Leu
 270 275 280
atc tta agc aag tgg ctg gaa cag gtg tac cca agc tcc gtg gag gaa 976
Ile Leu Ser Lys Trp Leu Glu Gln Val Tyr Pro Ser Ser Val Glu Glu
 285 290 295
gag gca aag ctg ttt ttg tgg tgg cac caa gtc ctt cag ctc tcc ctc 1024
Glu Ala Lys Leu Phe Leu Trp Trp His Gln Val Leu Gln Leu Ser Leu
 300 305 310
att cag aca gag cag aat gac tcc gtc ctg aca gaa tct gtc att cga 1072
Ile Gln Thr Glu Gln Asn Asp Ser Val Leu Thr Glu Ser Val Ile Arg
315 320 325 330
att ctg ctc ttg gtt cag agc agg cag aac ctc gtg gct gag gag aga 1120
Ile Leu Leu Leu Val Gln Ser Arg Gln Asn Leu Val Ala Glu Glu Arg
 335 340 345
ctc agc tct ggg atc ctg ggg gca att ggg ttt ggc cgg aag tcg cct 1168
Leu Ser Ser Gly Ile Leu Gly Ala Ile Gly Phe Gly Arg Lys Ser Pro
 350 355 360
ttg tct aac agg ttc cga gtg gtt gcc cga agc atg gct gcc ttc ctt 1216
Leu Ser Asn Arg Phe Arg Val Val Ala Arg Ser Met Ala Ala Phe Leu
 365 370 375

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 Ser Val Gln Val Pro Met Glu Asp Gln Ile Arg Leu Arg Pro Gly Ser
 380 385 390
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 Glu Leu His Leu Thr Pro Lys Ala Gln Gln Ala Leu Asn Ala Leu Glu
 395 400 405 410
 tcc atg gca tca agt aag cag tat gtt gaa tac cag gat caa ata ttg 1360
 Ser Met Ala Ser Ser Lys Gln Tyr Val Glu Tyr Gln Asp Gln Ile Leu
 415 420 425
 caa gcc acc caa ttt ata agg cat cct ggc cat tgc ctt caa gat ggg 1408
 Gln Ala Thr Gln Phe Ile Arg His Pro Gly His Cys Leu Gln Asp Gly
 430 435 440
 aaa agc ttc ttg gct ctt ctc gtt aac tgt ctg tat cca gaa gtg cat 1456
 Lys Ser Phe Leu Ala Leu Leu Val Asn Cys Leu Tyr Pro Glu Val His
 445 450 455
 tat ttg gac cac ata cga tagtta aactgaggc tcttgaaaaa cccattgctg 1510
 Tyr Leu Asp His Ile Arg
 460
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 aattttgggg tgtgtgtgtg tgtgtgtgtg tgttttctta gctcttaaga ccttctgggg 1690
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 tcaactcagta cccttacttt taaaccccat ttgtgttcct ccaaagtaaa gaagtcaatt 1930

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tctcagaagg gagataaaaa tgccgagtta gttaaagtgg gtcattgtga aaatacgacc 2050
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aagaaaattt gagaagctgt ggacaattta atagtctgat ctggcaacag cgatttttgt 3130
ttggaaatat ttgtgtttt ctttgaggag gatataatta ctgatatcct aggatgtgaa 3190
atttttgagt gacagtatgc acattttaaa gaaaattatg attaactctgt ataagtttt 3250
ttggtctgta aaaattataa aaaataaaat catttatctt tggttgt 3297

<210> 58

127/307

<211> 2126

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (61)... (1473)

<400> 58

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atg tct aga ctg gga gcc ctg ggt ggt gcc cgt gcc ggg ctg gga ctg      108
Met Ser Arg Leu Gly Ala Leu Gly Gly Ala Arg Ala Gly Leu Gly Leu
      1           5           10           15
ttg ctg ggt acc gcc gcc ggc ctt gga ttc ctg tgc ctc ctt tac agc      156
Leu Leu Gly Thr Ala Ala Gly Leu Gly Phe Leu Cys Leu Leu Tyr Ser
      20           25           30
cag cga tgg aaa cgg acc cag cgt cat ggc cgc agc cag agc ctg ccc      204
Gln Arg Trp Lys Arg Thr Gln Arg His Gly Arg Ser Gln Ser Leu Pro
      35           40           45
aac tcc ctg gac tat acg cag act tca gat ccc gga cgc cac gtg atg      252
Asn Ser Leu Asp Tyr Thr Gln Thr Ser Asp Pro Gly Arg His Val Met
      50           55           60
ctc ctg cgg gct gtc cca ggt ggg gct gga gat gcc tca gtg ctg ccc      300
Leu Leu Arg Ala Val Pro Gly Gly Ala Gly Asp Ala Ser Val Leu Pro
      65           70           75           80
agc ctt cca cgg gaa gga cag gag aag gtg ctg gac cgc ctg gac ttt      348
Ser Leu Pro Arg Glu Gly Gln Glu Lys Val Leu Asp Arg Leu Asp Phe

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128/307

85	90	95	
gtg ctg acc agc ctt gtg gcg ctg cgg cgg gag gtg gag gag ctg aga			396
Val Leu Thr Ser Leu Val Ala Leu Arg Arg Glu Val Glu Glu Leu Arg			
100	105	110	
agc agc ctg cga ggg ctt gcg ggg gag att gtt ggg gag gtc cga tgc			444
Ser Ser Leu Arg Gly Leu Ala Gly Glu Ile Val Gly Glu Val Arg Cys			
115	120	125	
cac atg gaa gag aac cag aga gtg gct cgg cgg cga agg ttt ccg ttt			492
His Met Glu Glu Asn Gln Arg Val Ala Arg Arg Arg Arg Phe Pro Phe			
130	135	140	
gtc cgg gag agg agt gac tcc act ggc tcc agc tct gtc tac ttc acg			540
Val Arg Glu Arg Ser Asp Ser Thr Gly Ser Ser Ser Val Tyr Phe Thr			
145	150	155	160
gcc tcc tcg gga gcc acg ttc aca gat gct gag agt gaa ggg ggt tac			588
Ala Ser Ser Gly Ala Thr Phe Thr Asp Ala Glu Ser Glu Gly Gly Tyr			
165	170	175	
aca aca gcc aat gcg gag tct gac aat gag cgg gac tct gac aaa gaa			636
Thr Thr Ala Asn Ala Glu Ser Asp Asn Glu Arg Asp Ser Asp Lys Glu			
180	185	190	
agt gag gac ggg gaa gat gaa gtg agc tgt gag act gtg aag atg ggg			684
Ser Glu Asp Gly Glu Asp Glu Val Ser Cys Glu Thr Val Lys Met Gly			
195	200	205	
aga aag gat tct ctt gac ttg gag gaa gag gca gct tca ggt gcc tcc			732
Arg Lys Asp Ser Leu Asp Leu Glu Glu Glu Ala Ala Ser Gly Ala Ser			
210	215	220	

129/307

agt gcc ctg gag gct gga ggt tcc tca ggc ttg gag gat gtg ctg ccc 780
 Ser Ala Leu Glu Ala Gly Gly Ser Ser Gly Leu Glu Asp Val Leu Pro
 225 230 235 240
 ctc ctg cag cag gcc gac gag ctg cac agg ggt gat gag caa ggc aag 828
 Leu Leu Gln Gln Ala Asp Glu Leu His Arg Gly Asp Glu Gln Gly Lys
 245 250 255
 cgg gag ggc ttc cag ctg ctg ctc aac aac aag ctg gtg tat gga agc 876
 Arg Glu Gly Phe Gln Leu Leu Leu Asn Asn Lys Leu Val Tyr Gly Ser
 260 265 270
 cgg cag gac ttt ctc tgg cgc ctg gcc cga gcc tac agt gac atg tgt 924
 Arg Gln Asp Phe Leu Trp Arg Leu Ala Arg Ala Tyr Ser Asp Met Cys
 275 280 285
 gag ctc act gag gag gtg agc gag aag aag tca tat gcc cta gat gga 972
 Glu Leu Thr Glu Glu Val Ser Glu Lys Lys Ser Tyr Ala Leu Asp Gly
 290 295 300
 aaa gaa gaa gca gag gct gct ctg gag aag ggg gat gag agt gct gac 1020
 Lys Glu Glu Ala Glu Ala Ala Leu Glu Lys Gly Asp Glu Ser Ala Asp
 305 310 315 320
 tgt cac ctg tgg tat gcg gtg ctt tgt ggt cag ctg gct gag cat gag 1068
 Cys His Leu Trp Tyr Ala Val Leu Cys Gly Gln Leu Ala Glu His Glu
 325 330 335
 agc atc cag agg cgc atc cag agt ggc ttt agc ttc aag gag cat gtg 1116
 Ser Ile Gln Arg Arg Ile Gln Ser Gly Phe Ser Phe Lys Glu His Val
 340 345 350
 gac aaa gcc att gct ctc cag cca gaa aac ccc atg gct cac ttt ctt 1164

130/307

Asp Lys Ala Ile Ala Leu Gln Pro Glu Asn Pro Met Ala His Phe Leu
 355 360 365
 ctt ggc agg tgg tgc tat cag gtc tct cac ctg agc tgg cta gaa aaa 1212
 Leu Gly Arg Trp Cys Tyr Gln Val Ser His Leu Ser Trp Leu Glu Lys
 370 375 380
 aaa act gct aca gcc ttg ctt gaa agc cct ctc agt gcc act gtg gaa 1260
 Lys Thr Ala Thr Ala Leu Leu Glu Ser Pro Leu Ser Ala Thr Val Glu
 385 390 395 400
 gat gcc ctc cag agc ttc cta aag gct gaa gaa cta cag cca gga ttt 1308
 Asp Ala Leu Gln Ser Phe Leu Lys Ala Glu Glu Leu Gln Pro Gly Phe
 405 410 415
 tcc aaa gca gga agg gta tat att tcc aag tgc tac aga gaa cta ggg 1356
 Ser Lys Ala Gly Arg Val Tyr Ile Ser Lys Cys Tyr Arg Glu Leu Gly
 420 425 430
 aaa aac tct gaa gct aga tgg tgg atg aag ttg gcc ctg gag ctg cca 1404
 Lys Asn Ser Glu Ala Arg Trp Trp Met Lys Leu Ala Leu Glu Leu Pro
 435 440 445
 gat gtc acg aag gag gat ttg gct atc cag aag gac ctg gaa gaa ctg 1452
 Asp Val Thr Lys Glu Asp Leu Ala Ile Gln Lys Asp Leu Glu Glu Leu
 450 455 460
 gaa gtc att tta cga gac taaccacgtt tcaactggcct tcatgacttg 1500
 Glu Val Ile Leu Arg Asp
 465 470
 atgccactat ttaagggtggg ggggcgggga ggcttttttc cttagacctt gctgagatca 1560
 ggaaaccaca caaatctgtc tcttgggtct gactgctacc cactaccact cccattagt 1620

131/307

taatttattc taacctctaa cctaattctag aattggggca gtactcatgg cttccgtttc 1680
 tgttggttctc tcccttgagt aatctcttaa aaaaatcaag attcacacct gccccaggat 1740
 tacacatggg tagagcctgc aagacctgag accttccaat tgctgggtgag gtggatgaac 1800
 ttcaaagcta taggaacaaa gcacataact tgcacttta atctttttca ctgactaata 1860
 ggactcagta catatagtct taagatcata ccttacctac caaggtaaaa agagggatca 1920
 gagtggccca cagacattgc tttcttatca cctatcatgt gaattctacc tgtattcctg 1980
 ggctggacca cttgataact tccagtgtcc tggcagcttt tggaatgaca gcagtggat 2040
 ggggtttatg atgctataaa acaatgtctg aaaagttgcc tagaatatat tttgttacia 2100
 acttgaaata aaccaaattt gatgtt 2126

<210> 59

<211> 1781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)... (805)

<400> 59

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 cccacaagga gca atg gag cag ggc agc ggc cgc ttg gag gac ttc cct 109
 Met Glu Gln Gly Ser Gly Arg Leu Glu Asp Phe Pro
 1 5 10
 gtc aat gtg ttc tcc gtc act cct tac aca ccc agc acc gct gac atc 157
 Val Asn Val Phe Ser Val Thr Pro Tyr Thr Pro Ser Thr Ala Asp Ile

15

20

25

132/307

cag gtg tcc gat gat gac aag gcg ggg gcc acc ttg ctc ttc tca ggc 205
Gln Val Ser Asp Asp Asp Lys Ala Gly Ala Thr Leu Leu Phe Ser Gly
30 35 40
atc ttt ctg gga ctg gtg ggg atc aca ttc act gtc atg ggc tgg atc 253
Ile Phe Leu Gly Leu Val Gly Ile Thr Phe Thr Val Met Gly Trp Ile
45 50 55 60
aaa tac caa ggt gtc tcc cac ttt gaa tgg acc cag ctc ctt ggg ccc 301
Lys Tyr Gln Gly Val Ser His Phe Glu Trp Thr Gln Leu Leu Gly Pro
65 70 75
gtc ctg ctg tca gtt ggg gtg aca ttc atc ctg att gct gtg tgc aag 349
Val Leu Leu Ser Val Gly Val Thr Phe Ile Leu Ile Ala Val Cys Lys
80 85 90
ttc aaa atg ctc tcc tgc cag ttg tgc aaa gaa agt gag gaa agg gtc 397
Phe Lys Met Leu Ser Cys Gln Leu Cys Lys Glu Ser Glu Glu Arg Val
95 100 105
ccg gac tgc gaa cag aca cca gga gga cca tca ttt gtt ttc act ggc 445
Pro Asp Ser Glu Gln Thr Pro Gly Gly Pro Ser Phe Val Phe Thr Gly
110 115 120
atc aac caa ccc atc acc ttc cat ggg gcc act gtg gtg cag tac atc 493
Ile Asn Gln Pro Ile Thr Phe His Gly Ala Thr Val Val Gln Tyr Ile
125 130 135 140
cct cct cct tat ggt tct cca gag cct atg ggg ata aat acc agc tac 541
Pro Pro Pro Tyr Gly Ser Pro Glu Pro Met Gly Ile Asn Thr Ser Tyr
145 150 155
ctg cag tct gtg gtg agc ccc tgc ggc ctc ata acc tct gga ggg gca 589

133/307

Leu Gln Ser Val Val Ser Pro Cys Gly Leu Ile Thr Ser Gly Gly Ala

160

165

170

gca gcc gcc atg tca agt cct cct caa tac tac acc atc tac cct caa 637

Ala Ala Ala Met Ser Ser Pro Pro Gln Tyr Tyr Thr Ile Tyr Pro Gln

175

180

185

gat aac tct gca ttt gtg gtt gat gag ggc tgc ctt tct ttc acg gac 685

Asp Asn Ser Ala Phe Val Val Asp Glu Gly Cys Leu Ser Phe Thr Asp

190

195

200

ggg gga aat cac agg ccc aat cct gat gtt gac cag cta gaa gag aca 733

Gly Gly Asn His Arg Pro Asn Pro Asp Val Asp Gln Leu Glu Glu Thr

205

210

215

220

cag ctg gaa gag gag gcc tgt gcc tgc ttc tct cct ccc cct tat gaa 781

Gln Leu Glu Glu Glu Ala Cys Ala Cys Phe Ser Pro Pro Pro Tyr Glu

225

230

235

gaa ata tac tct ctc cct cgc tagaggt attctgatat aataacacaa 830

Glu Ile Tyr Ser Leu Pro Arg

240

tgctcagctc agggagcaag tgtttccgtc attgttacct gacaaccgtg gtgttctatg 890

ttgtaacctt cagaagttac agcagcgccc aggcagcctg acagagatca ttcaaggggg 950

gaaaggggaa gtgggaggtg caatttctca gatttgtaaa aattaggtg ggctggggaa 1010

attctcctcc ggaacagttt caaattccct cgggtaagaa atctcctgta taaggttcag 1070

gagcaggaat ttacttttt catccaccac cctccccctt ctctgtagga aggcatgtgt 1130

ggctcaattt taacccagc agccaatgga aaaatcacga cttctgagac tttgggagtt 1190

tccacagagg tgagagtcgg gtgggaagga agcagggaag agaaagcagg cccagctgga 1250

gatttctctg tggtgtcct tggcccaaaa gcagactcac taatcccaaa caactcagct 1310

134/307

gccatctggc ctctctgagg actctgggta ccttaaagac tataaaacaa aacaaaacaa 1370
 aaacatcaaa ccaatgaaat aaaataaatc atgtctcctg ctagaatagt attggatacc 1430
 tgactaaatt acacaaaata gaccataata ggatagcact gtgaatacat ccttcccgat 1490
 cactgagtca cagtgaccct tggtgtctgc agttctcgtc tgcaagggtg aagcttgacg 1550
 tgtgatgaac atgggtgggc tcttgggtcca cccagcgtg gggcctgcgc caagcatgaa 1610
 ctagctggga ccagtggctg acagaacaca ggacttcctt aagtaccctg aggtccgtgg 1670
 agcaagacag agcagagttg ccattgtcaac acatggggaa tgatatgata gaaacaatct 1730
 ttatgactaa aagaaactca tcttcttcat taaaaaaact ttggtgtcct t 1781

<210> 60

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (87)... (899)

<400> 60

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 gcaccggggc gatcgggcga gtggcc atg gcg ggc gcc gag gac tgg ccg ggc 113

Met Ala Gly Ala Glu Asp Trp Pro Gly

1

5

cag cag ctg gag ctg gac gag gac gag gcg tct tgt tgc cgc tgg ggc 161
 Gln Gln Leu Glu Leu Asp Glu Asp Glu Ala Ser Cys Cys Arg Trp Gly

10

15

20

25

gcg cag cac gcc ggg gcc cgc gag ctg gct gcg ctc tac tcg cca ggc 209

135/307

Ala Gln His Ala Gly Ala Arg Glu Leu Ala Ala Leu Tyr Ser Pro Gly
 30 35 40
 aag cgc ctc cag gag tgg tgc tct gtg atc ctg tgc ttc agc ctc atc 257
 Lys Arg Leu Gln Glu Trp Cys Ser Val Ile Leu Cys Phe Ser Leu Ile
 45 50 55
 gcc cac aac ctg gtc cat ctc ctg ctg ctg gcc cgc tgg gag gac aca 305
 Ala His Asn Leu Val His Leu Leu Leu Leu Ala Arg Trp Glu Asp Thr
 60 65 70
 ccc ctc gtc ata ctc ggt gtt gtt gca ggg gct ctc att gct gac ttc 353
 Pro Leu Val Ile Leu Gly Val Val Ala Gly Ala Leu Ile Ala Asp Phe
 75 80 85
 ttg tct ggc ctg gta cac tgg ggt gct gac aca tgg ggc tct gtg gag 401
 Leu Ser Gly Leu Val His Trp Gly Ala Asp Thr Trp Gly Ser Val Glu
 90 95 100 105
 ctg ccc att gtg ggg aag gct ttc atc cga ccc ttc cgg gag cac cac 449
 Leu Pro Ile Val Gly Lys Ala Phe Ile Arg Pro Phe Arg Glu His His
 110 115 120
 att gac cca aca gct atc aca cgg cac gac ttc atc gag acc aac ggg 497
 Ile Asp Pro Thr Ala Ile Thr Arg His Asp Phe Ile Glu Thr Asn Gly
 125 130 135
 gac aac tgc ctg gtg aca ctg ctg ccg ctg cta aac atg gcc tac aag 545
 Asp Asn Cys Leu Val Thr Leu Leu Pro Leu Leu Asn Met Ala Tyr Lys
 140 145 150
 ttc cgc acc cac agc cct gaa gcc ctg gag cag cta tac ccc tgg gag 593
 Phe Arg Thr His Ser Pro Glu Ala Leu Glu Gln Leu Tyr Pro Trp Glu

136/307

155 160 165
tgc ttc gtc ttc tgc ctg atc atc ttc ggc acc ttc acc aac cag atc 641
Cys Phe Val Phe Cys Leu Ile Ile Phe Gly Thr Phe Thr Asn Gln Ile
170 175 180 185
cac aag tgg tgc cac acg tac ttt ggg ctg cca cgc tgg gtc acc ctc 689
His Lys Trp Ser His Thr Tyr Phe Gly Leu Pro Arg Trp Val Thr Leu
190 195 200
ctg cag gac tgg cat gtc atc ctg cca cgt aaa cac cat cgc atc cac 737
Leu Gln Asp Trp His Val Ile Leu Pro Arg Lys His His Arg Ile His
205 210 215
cac gtc tca ccc cac gag acc tac ttc tgc atc acc aca ggc tgg ctc 785
His Val Ser Pro His Glu Thr Tyr Phe Cys Ile Thr Thr Gly Trp Leu
220 225 230
aac tac cct ctg gag aag ata ggc ttc tgg cga cgc ctg gag gac ctc 833
Asn Tyr Pro Leu Glu Lys Ile Gly Phe Trp Arg Arg Leu Glu Asp Leu
235 240 245
atc cag ggc ctg acg ggc gag aag cct cgg gca gat gac atg aaa tgg 881
Ile Gln Gly Leu Thr Gly Glu Lys Pro Arg Ala Asp Asp Met Lys Trp
250 255 260 265
gcc cag aag atc aaa taac ttctccgagc ctgtacctg gttgcccaacc 930
Ala Gln Lys Ile Lys
270
ttccctagcc cccaaaccga agccatctgc caaattccag cctctttgag ctggccccc 990
cagatggaga ggacatctcc tgggctgggc ccaggtaccc cagcccaccc ctcatgacac 1050
agaataacttg agccactgat ttttcatttc ttttttttt tttttcctcg gccctctc 1110

137/307

agccacctga gttgctctat ctgcaagcct gactctgccca gcttcccctg gtagagagga 1170
 ggtttaccca ctccctgcac gctgcccgc cctgccccgc tgggcagccc ttcagtgtgg 1230
 ctggcggttg ggccagttag ttgcctcttt ccttcttgt ctggccccag tggcttgggg 1290
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 cccgggaggc tgggcaggtag gacagcccca gccaccacct tcagcctagc ctgtccccc 1410
 aggatggtga agctcagcag gggctctgagg gtagccggcc agaagaggct ggaacctcct 1470
 gctcaagtct agaccctac ttctctgctg cccccacct gccagagctg atgtttccaa 1530
 taccaagatg tttcacagg gcacagcccc tgcagagcat cttggtcatt tggaagagga 1590
 cacggtatcc cctctggcca gagtatgtca gagaaggaag agtagggctt tttgttttg 1650
 tttttttta aagggtcttg cttgtttaat gtaaataata gaaagccta atatcttttc 1710
 tgtaacacgg agtaatatat taatgtcatg ttttgatgt acataatata tttataacaa 1770
 agcagcaaga gtctactt 1788

<210> 61

<211> 389

<212> PRT

<213> Homo sapiens

<400> 61

Met Asp Arg Gly Glu Lys Ile Gln Leu Lys Arg Val Phe Gly Tyr Trp

1 5 10 15

Trp Gly Thr Ser Phe Leu Leu Ile Asn Ile Ile Gly Ala Gly Ile Phe

20 25 30

Val Ser Pro Lys Gly Val Leu Ala Tyr Ser Cys Met Asn Val Gly Val

35 40 45

Ser Leu Cys Val Trp Ala Gly Cys Ala Ile Leu Ala Met Thr Ser Thr

138/307

50 55 60
Leu Cys Ser Ala Glu Ile Ser Ile Ser Phe Pro Cys Ser Gly Ala Gln
65 70 75 80
Tyr Tyr Phe Leu Lys Arg Tyr Phe Gly Ser Thr Val Ala Phe Leu Asn
85 90 95
Leu Trp Thr Ser Leu Phe Leu Gly Ser Gly Val Val Ala Gly Gln Ala
100 105 110
Leu Leu Leu Ala Glu Tyr Ser Ile Gln Pro Phe Phe Pro Ser Cys Ser
115 120 125
Val Pro Lys Leu Pro Lys Lys Cys Leu Ala Leu Ala Met Leu Trp Ile
130 135 140
Val Gly Ile Leu Thr Ser Arg Gly Val Lys Glu Val Thr Trp Leu Gln
145 150 155 160
Ile Ala Ser Ser Val Leu Lys Val Ser Ile Leu Ser Phe Ile Ser Leu
165 170 175
Thr Gly Val Val Phe Leu Ile Arg Gly Lys Lys Glu Asn Val Glu Arg
180 185 190
Phe Gln Asn Ala Phe Asp Ala Glu Leu Pro Asp Ile Ser His Leu Ile
195 200 205
Gln Ala Ile Phe Gln Gly Tyr Phe Ala Tyr Ser Gly Glu Leu Lys Lys
210 215 220
Pro Arg Thr Thr Ile Pro Lys Cys Ile Phe Thr Ala Leu Pro Leu Val
225 230 235 240
Thr Val Val Tyr Leu Leu Val Asn Ile Ser Tyr Leu Thr Val Leu Thr
245 250 255

139/307

Pro Arg Glu Ile Leu Ser Ser Asp Ala Val Ala Ile Thr Trp Ala Asp

260

265

270

Arg Ala Phe Pro Ser Leu Ala Trp Ile Met Pro Phe Ala Ile Ser Thr

275

280

285

Ser Leu Phe Ser Asn Leu Leu Ile Ser Ile Phe Lys Ser Ser Arg Pro

290

295

300

Ile Tyr Leu Ala Ser Gln Glu Gly Gln Leu Pro Leu Leu Phe Asn Thr

305

310

315

320

Leu Asn Ser His Ser Ser Pro Phe Thr Ala Val Leu Leu Leu Val Thr

325

330

335

Leu Gly Ser Leu Ala Ile Ile Leu Thr Ser Leu Ile Asp Leu Ile Asn

340

345

350

Tyr Ile Phe Phe Thr Gly Ser Leu Trp Ser Ile Leu Leu Met Ile Gly

355

360

365

Ile Leu Arg Arg Arg Tyr Gln Glu Pro Asn Leu Ser Ile Pro Tyr Lys

370

375

380

Val Lys Leu Asp Phe

385

<210> 62

<211> 348

<212> PRT

<213> Homo sapiens

<400> 62

Met Ala Ala Thr Leu Gly Pro Leu Gly Ser Trp Gln Gln Trp Arg Arg

140/307

1 5 10 15
Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu Leu
20 25 30
Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly Gln Thr Phe
35 40 45
Glu Tyr Leu Lys Arg Glu His Ser Leu Ser Lys Pro Tyr Gln Gly Val
50 55 60
Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu Met Gly Asn Ala Met Val
65 70 75 80
Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp Met Gln Ser Lys Gln Gly
85 90 95
Ala Leu Trp Asn Arg Val Pro Cys Phe Leu Arg Asp Trp Glu Leu Gln
100 105 110
Val His Phe Lys Ile His Gly Gln Gly Lys Lys Asn Leu His Gly Asp
115 120 125
Gly Leu Ala Ile Trp Tyr Thr Lys Asp Arg Met Gln Pro Gly Pro Val
130 135 140
Phe Gly Asn Met Asp Lys Phe Val Gly Leu Gly Val Phe Val Asp Thr
145 150 155 160
Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg Val Phe Pro Tyr Ile Ser
165 170 175
Ala Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Glu Arg Asp Gly
180 185 190
Arg Pro Thr Glu Leu Gly Gly Cys Thr Ala Ile Val Arg Asn Leu His
195 200 205

141/307

Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile

210

215

220

Met Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val

225

230

235

240

Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser Ile

245

250

255

Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys Leu Phe

260

265

270

Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu Lys Leu His Arg Asp

275

280

285

Val Phe Leu Pro Ser Val Asp Asn Met Lys Leu Pro Glu Met Thr Ala

290

295

300

Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe Leu Ile Val Phe Phe

305

310

315

320

Ser Leu Val Phe Ser Val Phe Ala Ile Val Ile Gly Ile Ile Leu Tyr

325

330

335

Asn Lys Trp Gln Glu Gln Ser Arg Lys Arg Phe Tyr

340

345

<210> 63

<211> 261

<212> PRT

<213> Homo sapiens

<400> 63

Met Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys

142/307

1 5 10 15
Ser Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val
20 25 30
Val Thr Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu
35 40 45
Gln Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Pro Lys Gly Thr
50 55 60
Ile Thr Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Thr Phe
65 70 75 80
Leu Thr Ser Lys Asp Glu Gly Leu Lys Ala Thr Thr Thr Asp Val Arg
85 90 95
Lys Asn Asp Ser Ile Ile Ser Asn Val Thr Val Thr Ser Val Thr Leu
100 105 110
Pro Asn Ala Val Ser Thr Leu Gln Ser Ser Lys Pro Lys Thr Glu Thr
115 120 125
Gln Ser Ser Ile Lys Thr Thr Glu Ile Pro Gly Ser Val Leu Gln Pro
130 135 140
Asp Ala Ser Pro Ser Lys Thr Gly Thr Leu Thr Ser Ile Pro Val Thr
145 150 155 160
Ile Pro Glu Asn Thr Ser Gln Ser Gln Val Ile Gly Thr Glu Gly Gly
165 170 175
Lys Asn Ala Ser Thr Ser Ala Thr Ser Arg Ser Tyr Ser Ser Ile Ile
180 185 190
Leu Pro Val Val Ile Ala Leu Ile Val Ile Thr Leu Ser Val Phe Val
195 200 205

143/307

Leu Val Gly Leu Tyr Arg Met Cys Trp Lys Ala Asp Pro Gly Thr Pro

210 215 220

Glu Asn Gly Asn Asp Gln Pro Gln Ser Asp Lys Glu Ser Val Lys Leu

225 230 235 240

Leu Thr Val Lys Thr Ile Ser His Glu Ser Gly Glu His Ser Ala Gln

245 250 255

Gly Lys Thr Lys Asn

260

<210> 64

<211> 222

<212> PRT

<213> Homo sapiens

<400> 64

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala Glu Leu

1 5 10 15

Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser Ile Arg

20 25 30

Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn Glu Glu Tyr

35 40 45

Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys Val Pro Asn Arg

50 55 60

Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys Asn Val Thr Gln Arg

65 70 75 80

Val Ser Phe Trp Phe Val Val Thr Asp Pro Ser Lys Asn His Thr Leu

144/307

85 90 95
Pro Ala Val Glu Val Gln Ser Ala Ile Arg Met Asn Lys Asn Arg Ile
100 105 110
Asn Asn Ala Phe Phe Leu Asn Asp Gln Thr Leu Glu Phe Leu Lys Ile
115 120 125
Pro Ser Thr Leu Ala Pro Pro Met Asp Pro Ser Val Pro Ile Trp Ile
130 135 140
Ile Ile Phe Gly Val Ile Phe Cys Ile Ile Ile Val Ala Ile Ala Leu
145 150 155 160
Leu Ile Leu Ser Gly Ile Trp Gln Arg Arg Arg Lys Asn Lys Glu Pro
165 170 175
Ser Glu Val Asp Asp Ala Glu Asp Lys Cys Glu Asn Met Ile Thr Ile
180 185 190
Glu Asn Gly Ile Pro Ser Asp Pro Leu Asp Met Lys Gly Gly His Ile
195 200 205
Asn Asp Ala Phe Met Thr Glu Asp Glu Arg Leu Thr Pro Leu
210 215 220

<210> 65

<211> 183

<212> PRT

<213> Homo sapiens

<400> 65

Met Gly Val Arg Val His Val Val Ala Ala Ser Ala Leu Leu Tyr Phe

1 5 10 15

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Ile Leu Leu Ser Gly Thr Arg Cys Glu Glu Asn Cys Gly Asn Pro Glu
20 25 30
His Cys Leu Thr Thr Asp Trp Val His Leu Trp Tyr Ile Trp Leu Leu
35 40 45
Val Val Ile Gly Ala Leu Leu Leu Cys Gly Leu Thr Ser Leu Cys
50 55 60
Phe Arg Cys Cys Cys Leu Ser Arg Gln Gln Asn Gly Glu Asp Gly Gly
65 70 75 80
Pro Pro Pro Cys Glu Val Thr Val Ile Ala Phe Asp His Asp Ser Thr
85 90 95
Leu Gln Ser Thr Ile Thr Ser Leu Gln Ser Val Phe Gly Pro Ala Ala
100 105 110
Arg Arg Ile Leu Ala Val Ala His Ser His Ser Ser Leu Gly Gln Leu
115 120 125
Pro Ser Ser Leu Asp Thr Leu Pro Gly Tyr Glu Glu Ala Leu His Met
130 135 140
Ser Arg Phe Thr Val Ala Met Cys Gly Gln Lys Ala Pro Asp Leu Pro
145 150 155 160
Pro Val Pro Glu Glu Lys Gln Leu Pro Pro Thr Glu Lys Glu Ser Thr
165 170 175
Arg Ile Val Asp Ser Trp Asn

180

<210> 66

<211> 262

146/307

<212> PRT

<213> Homo sapiens

<400> 66

Met Gly Lys Thr Phe Ser Gln Leu Gly Ser Trp Arg Glu Asp Glu Asn

1 5 10 15

Lys Ser Ile Leu Ser Ser Lys Pro Ala Ile Gly Ser Lys Ala Val Asn

20 25 30

Tyr Ser Ser Thr Gly Ser Ser Lys Ser Phe Cys Ser Cys Val Pro Cys

35 40 45

Glu Gly Thr Ala Asp Ala Ser Phe Val Thr Cys Pro Thr Cys Gln Gly

50 55 60

Ser Gly Lys Ile Pro Gln Glu Leu Glu Lys Gln Leu Val Ala Leu Ile

65 70 75 80

Pro Tyr Gly Asp Gln Arg Leu Lys Pro Lys His Thr Lys Leu Phe Val

85 90 95

Phe Leu Ala Val Leu Ile Cys Leu Val Thr Ser Ser Phe Ile Val Phe

100 105 110

Phe Leu Phe Pro Arg Ser Val Ile Val Gln Pro Ala Gly Leu Asn Ser

115 120 125

Ser Thr Val Ala Phe Asp Glu Ala Asp Ile Tyr Leu Asn Ile Thr Asn

130 135 140

Ile Leu Asn Ile Ser Asn Gly Asn Tyr Tyr Pro Ile Met Val Thr Gln

145 150 155 160

Leu Thr Leu Glu Val Leu His Leu Ser Leu Val Val Gly Gln Val Ser

165 170 175

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Asn Asn Leu Leu Leu His Ile Gly Pro Leu Ala Ser Glu Gln Met Phe

180

185

190

Tyr Ala Val Ala Thr Lys Ile Arg Asp Glu Asn Thr Tyr Lys Ile Cys

195

200

205

Thr Trp Leu Glu Ile Lys Val His His Val Leu Leu His Ile Gln Gly

210

215

220

Thr Leu Thr Cys Ser Tyr Leu Ser His Ser Glu Gln Leu Val Phe Gln

225

230

235

240

Ser Tyr Glu Tyr Val Asp Cys Arg Gly Asn Ala Ser Val Pro His Gln

245

250

255

Leu Thr Pro His Pro Pro

260

<210> 67

<211> 168

<212> PRT

<213> Homo sapiens

<400> 67

Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly Ser

1

5

10

15

Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Lys Asp Ala Pro

20

25

30

Ser Asn Cys Val Val Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile

35

40

45

Thr Ala Ala Ala Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys

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50 55 60
Leu Pro Leu Ile Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser
65 70 75 80
Asn Arg Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly
85 90 95
Ile Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro
100 105 110
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro
115 120 125
Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser
130 135 140
Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp Pro Val Pro
145 150 155 160
Asp Ser Pro Asn Phe Glu Val Ile
165

<210> 68

<211> 243

<212> PRT

<213> Homo sapiens

<400> 68

Met Ser Ser Gly Thr Glu Leu Leu Trp Pro Gly Ala Ala Leu Leu Val

1 5 10 15

Leu Leu Gly Val Ala Ala Ser Leu Cys Val Arg Cys Ser Arg Pro Gly

20 25 30

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Ala Lys Arg Ser Glu Lys Ile Tyr Gln Gln Arg Ser Leu Arg Glu Asp

35

40

45

Gln Gln Ser Phe Thr Gly Ser Arg Thr Tyr Ser Leu Val Gly Gln Ala

50

55

60

Trp Pro Gly Pro Leu Ala Asp Met Ala Pro Thr Arg Lys Asp Lys Leu

65

70

75

80

Leu Gln Phe Tyr Pro Ser Leu Glu Asp Pro Ala Ser Ser Arg Tyr Gln

85

90

95

Asn Phe Ser Lys Gly Ser Arg His Gly Ser Glu Glu Ala Tyr Ile Asp

100

105

110

Pro Ile Ala Met Glu Tyr Tyr Asn Trp Gly Arg Phe Ser Lys Pro Pro

115

120

125

Glu Asp Asp Asp Ala Asn Ser Tyr Glu Asn Val Leu Ile Cys Lys Gln

130

135

140

Lys Thr Thr Glu Thr Gly Ala Gln Gln Glu Gly Ile Gly Gly Leu Cys

145

150

155

160

Arg Gly Asp Leu Ser Leu Ser Leu Ala Leu Lys Thr Gly Pro Thr Ser

165

170

175

Gly Leu Cys Pro Ser Ala Ser Pro Glu Glu Asp Glu Glu Ser Glu Asp

180

185

190

Tyr Gln Asn Ser Ala Ser Ile His Gln Trp Arg Glu Ser Arg Lys Val

195

200

205

Met Gly Gln Leu Gln Arg Glu Ala Ser Pro Gly Pro Val Gly Ser Pro

210

215

220

Asp Glu Glu Asp Gly Glu Pro Asp Tyr Val Asn Gly Glu Val Ala Ala

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225 230 235 240

Thr Glu Ala

<210> 69

<211> 428

<212> PRT

<213> Homo sapiens

<400> 69

Met Ala Arg Ser Leu Cys Pro Gly Ala Trp Leu Arg Lys Pro Tyr Tyr

1 5 10 15

Leu Gln Ala Arg Phe Ser Tyr Val Arg Met Lys Tyr Leu Phe Phe Ser

20 25 30

Trp Leu Val Val Phe Val Gly Ser Trp Ile Ile Tyr Val Gln Tyr Ser

35 40 45

Thr Tyr Thr Glu Leu Cys Arg Gly Lys Asp Cys Lys Lys Ile Ile Cys

50 55 60

Asp Lys Tyr Lys Thr Gly Val Ile Asp Gly Pro Ala Cys Asn Ser Leu

65 70 75 80

Cys Val Thr Glu Thr Leu Tyr Phe Gly Lys Cys Leu Ser Thr Lys Pro

85 90 95

Asn Asn Gln Met Tyr Leu Gly Ile Trp Asp Asn Leu Pro Gly Val Val

100 105 110

Lys Cys Gln Met Glu Gln Ala Leu His Leu Asp Phe Gly Thr Glu Leu

115 120 125

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Glu Pro Arg Lys Glu Ile Val Leu Phe Asp Lys Pro Thr Arg Gly Thr

130

135

140

Thr Val Gln Lys Phe Lys Glu Met Val Tyr Ser Leu Phe Lys Ala Lys

145

150

155

160

Leu Gly Asp Gln Gly Asn Leu Ser Glu Leu Val Asn Leu Ile Leu Thr

165

170

175

Val Ala Asp Gly Asp Lys Asp Gly Gln Val Ser Leu Gly Glu Ala Lys

180

185

190

Ser Ala Trp Ala Leu Leu Gln Leu Asn Glu Phe Leu Leu Met Val Ile

195

200

205

Leu Gln Asp Lys Glu His Thr Pro Lys Leu Met Gly Phe Cys Gly Asp

210

215

220

Leu Tyr Val Met Glu Ser Val Glu Tyr Thr Ser Leu Tyr Gly Ile Ser

225

230

235

240

Leu Pro Trp Val Ile Glu Leu Phe Ile Pro Ser Gly Phe Arg Arg Ser

245

250

255

Met Asp Gln Leu Phe Thr Pro Ser Trp Pro Arg Lys Ala Lys Ile Ala

260

265

270

Ile Gly Leu Leu Glu Phe Val Glu Asp Val Phe His Gly Pro Tyr Gly

275

280

285

Asn Phe Leu Met Cys Asp Thr Ser Ala Lys Asn Leu Gly Tyr Asn Asp

290

295

300

Lys Tyr Asp Leu Lys Met Val Asp Met Arg Lys Ile Val Pro Glu Thr

305

310

315

320

Asn Leu Lys Glu Leu Ile Lys Asp Arg His Cys Glu Ser Asp Leu Asp

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325 330 335
Cys Val Tyr Gly Thr Asp Cys Arg Thr Ser Cys Asp Gln Ser Thr Met
340 345 350
Lys Cys Thr Ser Glu Val Ile Gln Pro Asn Leu Ala Lys Ala Cys Gln
355 360 365
Leu Leu Lys Asp Tyr Leu Leu Arg Gly Ala Pro Ser Glu Ile Arg Glu
370 375 380
Glu Leu Glu Lys Gln Leu Tyr Ser Cys Ile Ala Leu Lys Val Thr Ala
385 390 395 400
Asn Gln Met Glu Met Glu His Ser Leu Ile Leu Asn Asn Leu Lys Thr
405 410 415
Leu Leu Trp Lys Lys Ile Ser Tyr Thr Asn Asp Ser
420 425

<210> 70

<211> 283

<212> PRT

<213> Homo sapiens

<400> 70

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His

1 5 10 15

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr

20 25 30

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val

35 40 45

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Leu His Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys

50

55

60

Ser Leu Ala Glu Glu Leu His His Ile His Ser Arg Tyr Arg Gly Ser

65

70

75

80

Tyr Trp Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly

85

90

95

Ala Leu Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala

100

105

110

Val Gly Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln

115

120

125

Ala Leu Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile

130

135

140

Ser Ala Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala

145

150

155

160

Trp Ser Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln

165

170

175

Ala Arg Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly

180

185

190

Ala Val Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val

195

200

205

Pro Asp Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys

210

215

220

Leu Pro Gln Gln Thr Ala Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr

225

230

235

240

Ser Asn Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Asn Leu Gln

154/307

245 250 255
Met Thr Ala Ala Ser Arg Cys Pro Arg Arg Phe Ser Gly Thr Cys Gly
260 265 270
Arg Arg Lys Arg Lys Arg Leu Leu Trp Ala Ala
275 280

<210> 71

<211> 1167

<212> DNA

<213> Homo sapiens

<400> 71

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tactcttgca tgaacgtggg agtctccctg tgcgtttggg ctggctgtgc catactggcc 180
atgacatcaa ctctttgctc tgcagagata agtataagct tcccatgcag tggagctcaa 240
tactattttc tcaagagata ctttggtctc acggttgctt tttgaaatct ctggacatcc 300
ttgtttctgg ggtcaggggt agttgctggc caagctctgc tccttgctga gtacagcatc 360
cagccttttt tcccagctg ctctgtccca aagctgccta agaaatgtct ggcattggcc 420
atgttggtga tttaggaat tctgacttct cgtggtgtga aagaagtac ttggcttcag 480
atagctagct cagtgtgaa agtgtccata cttagcttca tttccctaac tggagtagtg 540
ttcctgataa gagggaaaaa ggagaatgta gaacgatttc agaatgcttt tgatgtgaa 600
cttcagata tctctcacct tatacaagcc atcttccaag gatattttgc atattcaggg 660
gagctgaaga agcccagaac aacaattccc aatgcatat ttactgcgtt acctctggtg 720
actgtagttt atttactggt taacatttcc tatctgactg ttctgacacc cagggaatt 780
ctctcttcag atgtgtagc tatcacatgg gctgatcgag cttttccctc attagcatgg 840

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attatgcctt ttgctatttc tacctcatta tttagcaacc ttctgatttc tatatttaaa 900
tcttcgagac caatatatct tgcaagccaa gagggccagc tgcctttgct atttaataca 960
cttaatagtc actcttctcc atttacagct gtgctactac ttgtcacttt gggatccctt 1020
gcaattatct taacaagtct aattgatttg ataaactata tttttttcac gggttcatta 1080
tggtctatat tattaatgat aggaatacta aggcggagat accaggaacc caatctatct 1140
ataccttata aggtaaaatt ggatttc 1167

<210> 72

<211> 1044

<212> DNA

<213> Homo sapiens

<400> 72

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cgggatgggt ccaggatgtt actccttctt cttttgttgg ggtctgggca ggggccacag 120
caagtcgggg cgggtcaaac gttcgagtac ttgaaacggg agcactcgct gtcgaagccc 180
taccagggtg tgggcacagg cagttcctca ctgtggaatc tgatgggcaa tgccatggtg 240
atgaccagat atatccgct taccocagat atgcaaagta aacagggtgc cttgtggaac 300
cgggtgccat gtttcctgag agactgggag ttgcagggtgc acttcaaaat ccatggacaa 360
ggaaagaaga atctgcatgg ggatggcttg gcaatctggt acacaaagga tcggatgcag 420
ccagggcctg tgtttgaaa catggacaaa tttgtggggc tgggagtatt ttagacacc 480
taccccaatg aggagaagca gcaagagcgg gtattccctt acatctcagc catggtgaac 540
aacggctccc tcagctatga tcatgagcgg gatgggcggc ctacagagct gggaggctgc 600
acagccattg tccgcaatct tcattacgac accttcctgg tgattcgcta cgtcaagagg 660
catttgacga taatgatgga tattgatgga aagcatgagt ggagggactg cattgaagtg 720
cccggagtcc gcctgccccg cggtactac ttcggcacct cctccatcac tggggatctc 780

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tcagataatc atgatgtcat ttccttgaag ttgtttgaac tgacagtga gagaacccca 840
 gaagaggaaa agctccatcg agatgtgttc ttgccctcag tggacaatat gaagctgcct 900
 gagatgacag ctccactgcc gcccttgagt ggcttgccc tcttcctcat cgtctttttc 960
 tccctggtgt tttctgtatt tgccatagtc attggtatca tactctacaa caaatggcag 1020
 gaacagagcc gaaagcgctt ctac 1044

<210> 73

<211> 783

<212> DNA

<213> Homo sapiens

<400> 73

atggaactgc ttcaagtga cttctttttt cttctgcca gtatttgag cagtaacagc 60
 acaggtgttt tagaggcagc taataattca cttgttgta ctacaacaaa accatctata 120
 acaacaccaa acacagaatc attacagaaa aatgttgta caccaacaac tggaacaact 180
 cctaaaggaa caatcaccaa tgaattactt aaaatgtctc tgatgtcaac agctactttt 240
 ttaacaagta aagatgaagg attgaaagcc acaaccactg atgtcaggaa gaatgactcc 300
 atcatttcaa acgtaacagt aacaagtgtt acatttcaa atgtgtttc aacattacaa 360
 agttccaaac ccaagactga aactcagagt tcaattaaaa caacagaaat accaggtagt 420
 gttctacaac cagatgcac acccttctaaa actggtacat taacctcaat accagttaca 480
 attccagaaa acacctcaca gtctcaagta ataggcactg aggggtgaaa aaatgcaagc 540
 acttcagcaa ccagccggtc ttattccagt attattttgc cgggtggtat tgctttgatt 600
 gtaataacac tttcagtatt tgttctggtg gggttggtacc gaatgtgctg gaaggcagat 660
 ccgggcacac cagaaaatgg aaatgatcaa cctcagctctg ataaagagag cgtgaagctt 720
 cttaccgtta agacaatttc tcatgagtct ggtgagcact ctgcacaagg aaaaaccaag 780
 aac 783

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<210> 74

<211> 666

<212> DNA

<213> Homo sapiens

<400> 74

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atgttgtggc tgctcttttt tctggtgact gccattcatg ctgaactctg tcaaccaggt      60
gcagaaaatg cttttaagt gagacttagt atcagaacag ctctgggaga taaagcatat      120
gcctgggata ccaatgaaga atacctcttc aaagcgatgg tagctttctc catgagaaaa      180
gttcccaaca gagaagcaac agaaatttcc catgtcctac tttgcaatgt aaccagagg      240
gtatcattct ggtttgtggt tacagaccct tcaaaaaatc acacccttcc tgctgttgag      300
gtgcaatcag ccataagaat gaacaagaac cggatcaaca atgccttctt tctaatgac      360
caaactctgg aatttttaaa aatcccttcc acacttgac caccatgga cccatctgtg      420
cccatctgga ttattatatt tgggtgata tttgcatca tcatagttgc aattgcacta      480
ctgattttat cagggatctg gcaacgtaga agaaagaaca aagaaccatc tgaagtggat      540
gacgctgaag ataagtgtga aaacatgatc acaattgaaa atggcatccc ctctgatccc      600
ctggacatga agggagggca tattaatgat gccttcatga cagaggatga gaggctcacc      660
cctctc
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<210> 75

<211> 549

<212> DNA

<213> Homo sapiens

<400> 75

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atgggagtcc gagttcatgt cgtggcggcc tcagccctgc tgtatttcat cctgctttct      60
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158/307

gggacgagat gtgaggaaaa ctgtggtaat cctgaacatt gcctgaccac agactgggta 120
catctctggt atatatggtt gctagtggta attggcgcgc tgcttctcct gtgtggcctg 180
acgtccctgt gcttccgctg ctgctgtctg agccgccagc aaaatgggga agatgggggc 240
ccaccaccct gtgaagtgaac cgtcattgct ttgatcacg acagcactct ccagagcact 300
atcacatctc tgcagtcggt gtttggccct gcagctcgga ggatcctggc tgtggctcac 360
tcccacagct ccttgggcca gctgccctcc tctttggaca ccctcccagg gtatgaagaa 420
gctcttcaca tgagtcgctt cacagtagcc atgtgcgggc agaaagcacc tgatctaccc 480
ccagtacctg aagaaaagca gctgcctcca acagagaagg agtcgactcg aatagttgac 540
tcttggaaac 549

<210> 76

<211> 786

<212> DNA

<213> Homo sapiens

<400> 76

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tcctccaaac cagccattgg cagcaaggct gtcaactact ccagcaccgg tagcagcaag 120
tctttttgtt cctgtgtgcc ttgtgaagga actgctgatg ccagcttcgt gacttgtccc 180
acctgccagg gcagtggcaa gattcccca gagctggaga agcagttggt ggctctcatt 240
ccctatgggg accagaggct gaagcccaag cacacgaagc tctttgtgtt cctggccgtg 300
ctcatctgcc tggtagacct ctccttcac gtctttttcc tgtttccccg gtccgtcatt 360
gtgcagcctg caggcctcaa ctctccaca gtggcctttg atgaggctga tatctacctc 420
aacataacga atatcttaaa catctccaat ggcaactact accccattat ggtgacacag 480
ctgaccctcg aggttctgca cctgtccctc gtggtggggc aggtttccaa caaccttctc 540
ctacacattg gccctttggc cagtgaacag atgttttacg cagtagctac caagatacgg 600

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gatgaaaaca catacaaaat ctgtacctgg ctggaaatca aagtccacca tgtgcttttg 660
 cacatccagg gcaccctgac ctgttcatac ctgagccatt cagagcagct ggtctttcag 720
 agctatgaat atgtggactg ccgaggaaac gcattctgtgc cccaccagct gacccctcac 780
 ccacca 786

<210> 77

<211> 504

<212> DNA

<213> Homo sapiens

<400> 77

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 ctcttctctgg ctgcgtccct aggcaaagat gcaccatcca actgtgtggt gtacccatcc 120
 tcctcccagg agagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcatcgta 180
 ggaatcctct gcctccccct catcctgtctc ctggtctaca agcaaaggca ggcagcctcc 240
 aaccgccgtg cccaggagct ggtgcggatg gacagcaaca ttcaagggat tgaaaacccc 300
 ggctttgaag cctcaccacc tgcccagggg atacccgagg ccaaagtcag gcacccctg 360
 tcctatgtgg cccagcggca gccttctgag tctgggcggc atctgcttc ggagcccagc 420
 accccctgt cctctccagg ccccgagac gtcttcttcc catcctgga ccctgtcct 480
 gactctccaa actttgaggt catc 504

<210> 78

<211> 729

<212> DNA

<213> Homo sapiens

<400> 78

160/307

atgagctcgg ggactgaaact gctgtggccc ggagcagcgc tgctgggtgct gttgggggtg 60
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 cagcagagaa gtctgcgtga ggaccaacag agctttacgg ggtcccggac ctactccttg 180
 gtggggcagg catggccagg acccctggcg gacatggcac ccacaaggaa ggacaagctg 240
 ttgaattct accccagcct ggaggatcca gcattctcca ggtaccagaa cttcagcaaa 300
 ggaagcagac acgggtcgga ggaagcctac atagacccca ttgccatgga gtattacaac 360
 tgggggcggt tctcgaagcc cccagaagat gatgatgcca attcctacga gaatgtgctc 420
 atttgcaagc agaaaaccac agagacaggt gccagcagg agggcatagg tggcctctgc 480
 agaggggacc tcagcctgtc actggccctg aagactggcc ccacttctgg tctctgtccc 540
 tctgcctccc cggaagaaga tgaggaatct gaggattatc agaactcagc atccatccat 600
 cagtggcgcg agtccaggaa ggtcatgggg caactccaga gagaagcacc ccctggcccc 660
 gtgggaagcc cagacgagga ggacggggaa ccggattacg tgaatgggga ggtggcagcc 720
 acagaagcc 729

<210> 79

<211> 1284

<212> DNA

<213> Homo sapiens

<400> 79

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 tggattatat atgtgcagta ttctacctat acagaattat gcagaggaaa ggactgtaag 180
 aaaataatat gtgacaagta caagactgga gttattgatg ggcctgcatg taacagcctt 240
 tgtgttacag aaactcttta ctttgaaaa tgtttatcca ccaagcccaa caatcagatg 300
 tatttaggga tttgggataa tctaccaggt gttgtgaaat gtcaaagga acaagcgtt 360

161/307

catcttgatt ttggaactga attggaacca agaaaagaaa tagtgctatt tgataagcca 420
actagaggaa ctactgtaca aaaatttaaa gaaatggtct atagtctctt taaggcaaaa 480
ttgggtgacc aaggaaacct ctctgaactg gttaatctca tcttgacggt ggctgatgga 540
gacaaagatg gccaggtttc cttgggagaa gcaaagtcgg catgggcact tcttcaactg 600
aatgaatttc ttctcatggt gatacttcaa gataaagaac atacccccaa attaatggga 660
ttctgtggtg acctctatgt gatggaaagt gtgaatata cctctcttta tggaataagc 720
cttccttggg tcattgaact tttattcca tctgggttca gaagaagcat ggatcagctg 780
ttcacaccat catggccaag aaaggccaaa atagccatag gacttctaga atttgtggaa 840
gatgttttcc atggccccta cggaaatttc ctcatgtgcg atactagtgc caaaaccta 900
ggatataatg ataagtatga ttgaaaatg gtggatatga gaaaattgt gccagagaca 960
aacctgaaag aacttattaa ggatcgtcac tgtgagtctg atttggactg tgtctatggc 1020
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ccaaacttgg caaaagcttg tcagttactc aaagactacc tactgcgtgg tgctccaagt 1140
gaaattcgtg aagaattaga aaagcagctt tattcttgta ttgctctcaa agtcacagca 1200
aatcaaattg aaatggaaca ttctttgata ctaaataacc taaaaacatt attgtggaag 1260
aaaatttccct acactaatga ctct 1284

<210> 80

<211> 849

<212> DNA

<213> Homo sapiens

<400> 80

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gagcacactc tccggtacct ggtgtccac ctagecctcc tgcagctggg actgctgtta 180

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aacggggtct gcagcctggc tgaggagctg caccacatcc actccaggta ccggggcagc 240
 tactggagga ctgtgcgggc ctgcctgggc tgccccctcc gccgtggggc cctgttgctg 300
 ctgtccatct atttctacta ctccctccca aatgcggtcg gcccgccctt cacttggatg 360
 ctgtccctcc tgggcctctc gcaggcactg aacatcctcc tgggcctcaa gggcctggcc 420
 ccagctgaga tctctgcagt gtgtgaaaaa gggaatttca acgtggccca tgggctggca 480
 tggatcatatt acatcgata tctgcggctg atcctgccag agtccaggc ccggattcga 540
 acttacaatc agcattacaa caacctgcta cggggtgcag tgagccagcg gctgtatatt 600
 ctccctccat tggactgtgg ggtgcctgat aacctgagta tggtgacct caacattcgc 660
 ttcttgata aactgcccc aagaccgct gaccgtgctg gcataagga tcgggtttac 720
 agcaacagca tctatgagct tctggagaac gggcagcgga acctgcagat gacagcagct 780
 tctcgtgtc ccaggagggt ctccggcacc tgcggcagga ggaaaaggaa gaggttactg 840
 tgggcagct 849

<210> 81

<211> 1376

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (100)... (1269)

<400> 81

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 attgtaattt atatagaatt ttaaaactct tcaattaca atg gat aga ggg gag 114

Met Asp Arg Gly Glu

1 5

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aaa ata cag ctc aag aga gtg ttt gga tat tgg tgg ggc aca agt ttt      162
Lys Ile Gln Leu Lys Arg Val Phe Gly Tyr Trp Trp Gly Thr Ser Phe
      10              15              20
ttg ctt att aat atc att ggt gca gga att ttt gtg tcc ccc aaa ggt      210
Leu Leu Ile Asn Ile Ile Gly Ala Gly Ile Phe Val Ser Pro Lys Gly
      25              30              35
gtg ttg gca tac tct tgc atg aac gtg gga gtc tcc ctg tgc gtt tgg      258
Val Leu Ala Tyr Ser Cys Met Asn Val Gly Val Ser Leu Cys Val Trp
      40              45              50
gct ggc tgt gcc ata ctg gcc atg aca tca act ctt tgc tct gca gag      306
Ala Gly Cys Ala Ile Leu Ala Met Thr Ser Thr Leu Cys Ser Ala Glu
      55              60              65
ata agt ata agc ttc cca tgc agt gga gct caa tac tat ttt ctc aag      354
Ile Ser Ile Ser Phe Pro Cys Ser Gly Ala Gln Tyr Tyr Phe Leu Lys
      70              75              80              85
aga tac ttt ggc tcc acg gtt gct ttt ttg aat ctc tgg aca tcc ttg      402
Arg Tyr Phe Gly Ser Thr Val Ala Phe Leu Asn Leu Trp Thr Ser Leu
      90              95              100
ttt ctg ggg tca ggg gta gtt gct ggc caa gct ctg ctc ctt gct gag      450
Phe Leu Gly Ser Gly Val Val Ala Gly Gln Ala Leu Leu Leu Ala Glu
      105              110              115
tac agc atc cag cct ttt ttt ccc agc tgc tct gtc cca aag ctg cct      498
Tyr Ser Ile Gln Pro Phe Phe Pro Ser Cys Ser Val Pro Lys Leu Pro
      120              125              130
aag aaa tgt ctg gca ttg gcc atg ttg tgg att gta gga att ctg act      546

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Lys Lys Cys Leu Ala Leu Ala Met Leu Trp Ile Val Gly Ile Leu Thr
 135 140 145
 tct cgt ggt gtg aaa gaa gtg act tgg ctt cag ata gct agc tca gtg 594
 Ser Arg Gly Val Lys Glu Val Thr Trp Leu Gln Ile Ala Ser Ser Val
 150 155 160 165
 ctg aaa gtg tcc ata ctt agc ttc att tcc cta act gga gta gtg ttc 642
 Leu Lys Val Ser Ile Leu Ser Phe Ile Ser Leu Thr Gly Val Val Phe
 170 175 180
 ctg ata aga ggg aaa aag gag aat gta gaa cga ttt cag aat gct ttt 690
 Leu Ile Arg Gly Lys Lys Glu Asn Val Glu Arg Phe Gln Asn Ala Phe
 185 190 195
 gat gct gaa ctt cca gat atc tct cac ctt ata caa gcc atc ttc caa 738
 Asp Ala Glu Leu Pro Asp Ile Ser His Leu Ile Gln Ala Ile Phe Gln
 200 205 210
 gga tat ttt gca tat tca ggg gag ctg aag aag ccc aga aca aca att 786
 Gly Tyr Phe Ala Tyr Ser Gly Glu Leu Lys Lys Pro Arg Thr Thr Ile
 215 220 225
 ccc aaa tgc ata ttt act gcg tta cct ctg gtg act gta gtt tat tta 834
 Pro Lys Cys Ile Phe Thr Ala Leu Pro Leu Val Thr Val Val Tyr Leu
 230 235 240 245
 ctg gtt aac att tcc tat ctg act gtt ctg aca ccc agg gaa att ctc 882
 Leu Val Asn Ile Ser Tyr Leu Thr Val Leu Thr Pro Arg Glu Ile Leu
 250 255 260
 tct tca gat gct gta gct atc aca tgg gct gat cga gct ttt ccc tca 930
 Ser Ser Asp Ala Val Ala Ile Thr Trp Ala Asp Arg Ala Phe Pro Ser

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265	270	275	
tta gca tgg att atg cct ttt gct att tct acc tca tta ttt agc aac			978
Leu Ala Trp Ile Met Pro Phe Ala Ile Ser Thr Ser Leu Phe Ser Asn			
280	285	290	
ctt ctg att tct ata ttt aaa tct tcg aga cca ata tat ctt gca agc			1026
Leu Leu Ile Ser Ile Phe Lys Ser Ser Arg Pro Ile Tyr Leu Ala Ser			
295	300	305	
caa gag ggc cag ctg cct ttg cta ttt aat aca ctt aat agt cac tct			1074
Gln Glu Gly Gln Leu Pro Leu Leu Phe Asn Thr Leu Asn Ser His Ser			
310	315	320	325
tct cca ttt aca gct gtg cta cta ctt gtc act ttg gga tcc ctt gca			1122
Ser Pro Phe Thr Ala Val Leu Leu Leu Val Thr Leu Gly Ser Leu Ala			
330	335	340	
att atc tta aca agt cta att gat ttg ata aac tat att ttt ttc acg			1170
Ile Ile Leu Thr Ser Leu Ile Asp Leu Ile Asn Tyr Ile Phe Phe Thr			
345	350	355	
ggc tca tta tgg tct ata tta tta atg ata gga ata cta agg cgg aga			1218
Gly Ser Leu Trp Ser Ile Leu Leu Met Ile Gly Ile Leu Arg Arg Arg			
360	365	370	
tac cag gaa ccc aat cta tct ata cct tat aag gta aaa ttg gat ttc			1266
Tyr Gln Glu Pro Asn Leu Ser Ile Pro Tyr Lys Val Lys Leu Asp Phe			
375	380	385	
taat tcttttctgt gtgaaataac agatattgag tataactgta ttttaagatta			1320
taatcagagc atctataagt agatcttctg aatactcagt tactgtgaaa cacatg			1376

166/307

<210> 82

<211> 2392

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)... (1068)

<400> 82

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                               Met Ala Ala Thr Leu Gly Pro Leu Gly Ser
                               1           5           10
tgg cag cag tgg cgg cga tgt ttg tgc gct cgg gat ggg tcc agg atg      99
Trp Gln Gln Trp Arg Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met
                               15           20           25
tta ctc ctt ctt ctt ttg ttg ggg tct ggg cag ggg cca cag caa gtc      147
Leu Leu Leu Leu Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val
                               30           35           40
ggg gcg ggt caa acg ttc gag tac ttg aaa cgg gag cac tcg ctg tcg      195
Gly Ala Gly Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu Ser
                               45           50           55
aag ccc tac cag ggt gtg ggc aca ggc agt tcc tca ctg tgg aat ctg      243
Lys Pro Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu
                               60           65           70
atg ggc aat gcc atg gtg atg acc cag tat atc cgc ctt acc cca gat      291
Met Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp

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75	80	85	90	
atg caa agt aaa cag ggt gcc ttg tgg aac cgg gtg cca tgt ttc ctg				339
Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe Leu				
	95	100	105	
aga gac tgg gag ttg cag gtg cac ttc aaa atc cat gga caa gga aag				387
Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln Gly Lys				
	110	115	120	
aag aat ctg cat ggg gat ggc ttg gca atc tgg tac aca aag gat cgg				435
Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr Lys Asp Arg				
	125	130	135	
atg cag cca ggg cct gtg ttt gga aac atg gac aaa ttt gtg ggg ctg				483
Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys Phe Val Gly Leu				
	140	145	150	
gga gta ttt gta gac acc tac ccc aat gag gag aag cag caa gag cgg				531
Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg				
	155	160	165	170
gta ttc ccc tac atc tca gcc atg gtg aac aac ggc tcc ctc agc tat				579
Val Phe Pro Tyr Ile Ser Ala Met Val Asn Asn Gly Ser Leu Ser Tyr				
	175	180	185	
gat cat gag cgg gat ggg cgg cct aca gag ctg gga ggc tgc aca gcc				627
Asp His Glu Arg Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Thr Ala				
	190	195	200	
att gtc cgc aat ctt cat tac gac acc ttc ctg gtg att cgc tac gtc				675
Ile Val Arg Asn Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val				
	205	210	215	

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aag agg cat ttg acg ata atg atg gat att gat ggc aag cat gag tgg 723
Lys Arg His Leu Thr Ile Met Met Asp Ile Asp Gly Lys His Glu Trp
220 225 230
agg gac tgc att gaa gtg ccc gga gtc cgc ctg ccc cgc ggc tac tac 771
Arg Asp Cys Ile Glu Val Pro Gly Val Arg Leu Pro Arg Glu Tyr Tyr
235 240 245 250
ttc ggc acc tcc tcc atc act ggg gat ctc tca gat aat cat gat gtc 819
Phe Gly Thr Ser Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val
255 260 265
att tcc ttg aag ttg ttt gaa ctg aca gtg gag aga acc cca gaa gag 867
Ile Ser Leu Lys Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu
270 275 280
gaa aag ctc cat cga gat gtg ttc ttg ccc tca gtg gac aat atg aag 915
Glu Lys Leu His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met Lys
285 290 295
ctg cct gag atg aca gct cca ctg ccg ccc ctg agt ggc ctg gcc ctc 963
Leu Pro Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu
300 305 310
ttc ctc atc gtc ttt ttc tcc ctg gtg ttt tct gta ttt gcc ata gtc 1011
Phe Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val
315 320 325 330
att ggt atc ata ctc tac aac aaa tgg cag gaa cag agc cga aag cgc 1059
Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys Arg
335 340 345
ttc tac tgagc cctcctgctg ccaccacttt tgtgactgtc acccatgagg 1110

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Phe Tyr

tatggaagga gcaggcactg gcctgagcat gcagcctgga gagtgttctt gtctctagca 1170
gctggttggg gactatattc tgtcactgga gttttgaatg cagggacccc gcattcccat 1230
ggttgtgcat ggggacatct aactctggtc tgggaagcca cccaccccag ggcaatgctg 1290
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attgcccaga gaagaaattt ggtttttttt ttcttaatgg acaagagaca gttgctgttc 2130
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tcttaaaatc accgatggaa cc 2392

<210> 83

170/307

<211> 1416

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (55)... (840)

<400> 83

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Met

1

gaa ctg ctt caa gtg acc att ctt ttt ctt ctg ccc agt att tgc agc 105

Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys Ser

5

10

15

agt aac agc aca ggt gtt tta gag gca gct aat aat tca ctt gtt gtt 153

Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val Val

20

25

30

act aca aca aaa cca tct ata aca aca cca aac aca gaa tca tta cag 201

Thr Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu Gln

35

40

45

aaa aat gtt gtc aca cca aca act gga aca act cct aaa gga aca atc 249

Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Pro Lys Gly Thr Ile

50

55

60

65

acc aat gaa tta ctt aaa atg tct ctg atg tca aca gct act ttt tta 297

Thr Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Thr Phe Leu

70

75

80

171/307

aca agt aaa gat gaa gga ttg aaa gcc aca acc act gat gtc agg aag	345
Thr Ser Lys Asp Glu Gly Leu Lys Ala Thr Thr Thr Asp Val Arg Lys	
85 90 95	
aat gac tcc atc att tca aac gta aca gta aca agt gtt aca ctt cca	393
Asn Asp Ser Ile Ile Ser Asn Val Thr Val Thr Ser Val Thr Leu Pro	
100 105 110	
aat gct gtt tca aca tta caa agt tcc aaa ccc aag act gaa act cag	441
Asn Ala Val Ser Thr Leu Gln Ser Ser Lys Pro Lys Thr Glu Thr Gln	
115 120 125	
agt tca att aaa aca aca gaa ata cca ggt agt gtt cta caa cca gat	489
Ser Ser Ile Lys Thr Thr Glu Ile Pro Gly Ser Val Leu Gln Pro Asp	
130 135 140 145	
gca tca cct tct aaa act ggt aca tta acc tca ata cca gtt aca att	537
Ala Ser Pro Ser Lys Thr Gly Thr Leu Thr Ser Ile Pro Val Thr Ile	
150 155 160	
cca gaa aac acc tca cag tct caa gta ata ggc act gag ggt gga aaa	585
Pro Glu Asn Thr Ser Gln Ser Gln Val Ile Gly Thr Glu Gly Gly Lys	
165 170 175	
aat gca agc act tca gca acc agc cgg tct tat tcc agt att att ttg	633
Asn Ala Ser Thr Ser Ala Thr Ser Arg Ser Tyr Ser Ser Ile Ile Leu	
180 185 190	
ccg gtg gtt att gct ttg att gta ata aca ctt tca gta ttt gtt ctg	681
Pro Val Val Ile Ala Leu Ile Val Ile Thr Leu Ser Val Phe Val Leu	
195 200 205	
gtg ggt ttg tac cga atg tgc tgg aag gca gat ccg ggc aca cca gaa	729

172/307

Val Gly Leu Tyr Arg Met Cys Trp Lys Ala Asp Pro Gly Thr Pro Glu
 210 215 220 225
 aat gga aat gat caa cct cag tct gat aaa gag agc gtg aag ctt ctt 777
 Asn Gly Asn Asp Gln Pro Gln Ser Asp Lys Glu Ser Val Lys Leu Leu
 230 235 240
 acc gtt aag aca att tct cat gag tct ggt gag cac tct gca caa gga 825
 Thr Val Lys Thr Ile Ser His Glu Ser Gly Glu His Ser Ala Gln Gly
 245 250 255
 aaa acc aag aac tga cagcttgagg aattctctcc acacctaggc aataattacg 880
 Lys Thr Lys Asn
 260
 cttaatcttc agcttctatg caccaagcgt ggaaaaggag aaagtctctgc agaatcaatc 940
 ccgacttcca tacctgctgc tggactgtac cagacgtctg tcccagtaaa gtgatgtcca 1000
 gtgacatgc aataatttga tggaatcaaa aagaaccccg gggctctcct gttctctcac 1060
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 <210> 84
 <211> 1347
 <212> DNA
 <213> Homo sapiens

173/307

<220>

<221> CDS

<222> (26)... (694)

<400> 84

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Met Leu Trp Leu Leu Phe Phe Leu Val

1

5

act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat gct ttt 100

Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn Ala Phe

10

15

20

25

aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca tat gcc 148

Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr Ala

30

35

40

tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct ttc tcc 196

Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe Ser

45

50

55

atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat gtc cta 244

Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val Leu

60

65

70

ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt aca gac 292

Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr Asp

75

80

85

cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca gcc ata 340

Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala Ile

90

95

100

105

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aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat gac caa 388
 Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp Gln
 110 115 120
 act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc atg gac 436
 Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro Met Asp
 125 130 135
 cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt tgc atc 484
 Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe Cys Ile
 140 145 150
 atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg caa cgt 532
 Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp Gln Arg
 155 160 165
 aga aga aag aac aaa gaa cca tct gaa gtg gat gac gct gaa gat aag 580
 Arg Arg Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu Asp Lys
 170 175 180 185
 tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat ccc ctg 628
 Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp Pro Leu
 190 195 200
 gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag gat gag 676
 Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu Asp Glu
 205 210 215
 agg ctc acc cct ctc tgaagggt gttgttctgc ttcctcaaga aattaaacat 730
 Arg Leu Thr Pro Leu
 220
 ttgtttctgt gtgactgtg agcatcctga aataccaaga gcagatcata tattttgttt 790

175/307

caccattctt cttttgtaat aaattttgaa tgtgcttgaa agtgaaaagc aatcaattat 850
 acccaccaac accactgaaa tcataagcta ttcacgactc aaaatattct aaaatatttt 910
 tctgacagta tagtgataa atgtggcat gtggtatttg tagttattga ttttaagcatt 970
 ttttagaaata agatcaggca tatgtatata ttttcacact tcaaagacct aaggaaaaat 1030
 aaattttcca gtggagaata catataatat ggtgtagaaa tcattgaaaa tggatccttt 1090
 ttgacgatca cttatatcac tctgtatatg actaagtaaa caaaagttag aagtaattat 1150
 tgtaaattga tggataaaaa tggaattact catatacagg gtggaatttt atcctgttat 1210
 cacaccaaca gttgattata tattttctga atatcagccc ctaataggac aattctattt 1270
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 atctcttttt gattgtg 1347

<210> 85

<211> 2284

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75)... (626)

<400> 85

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 aggaattcag cccg atg gga gtc cga gtt cat gtc gtg gcg gcc tca gcc 110
 Met Gly Val Arg Val His Val Val Ala Ala Ser Ala
 1 5 10
 ctg ctg tat ttc atc ctg ctt tct ggg acg aga tgt gag gaa aac tgt 158
 Leu Leu Tyr Phe Ile Leu Leu Ser Gly Thr Arg Cys Glu Glu Asn Cys

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15 20 25
 ggt aat cct gaa cat tgc ctg acc aca gac tgg gta cat ctc tgg tat 206
 Gly Asn Pro Glu His Cys Leu Thr Thr Asp Trp Val His Leu Trp Tyr
 30 35 40
 ata tgg ttg cta gtg gta att ggc gcg ctg ctt ctc ctg tgt ggc ctg 254
 Ile Trp Leu Leu Val Val Ile Gly Ala Leu Leu Leu Leu Cys Gly Leu
 45 50 55 60
 acg tcc ctg tgc ttc cgc tgc tgc tgt ctg agc cgc cag caa aat ggg 302
 Thr Ser Leu Cys Phe Arg Cys Cys Cys Leu Ser Arg Gln Gln Asn Gly
 65 70 75
 gaa gat ggg ggc cca cca ccc tgt gaa gtg acc gtc att gct ttc gat 350
 Glu Asp Gly Gly Pro Pro Pro Cys Glu Val Thr Val Ile Ala Phe Asp
 80 85 90
 cac gac agc act ctc cag agc act atc aca tct ctg cag tcg gtg ttt 398
 His Asp Ser Thr Leu Gln Ser Thr Ile Thr Ser Leu Gln Ser Val Phe
 95 100 105
 ggc cct gca gct cgg agg atc ctg gct gtg gct cac tcc cac agc tcc 446
 Gly Pro Ala Ala Arg Arg Ile Leu Ala Val Ala His Ser His Ser Ser
 110 115 120
 ctg ggc cag ctg ccc tcc tct ttg gac acc ctc cca ggg tat gaa gaa 494
 Leu Gly Gln Leu Pro Ser Ser Leu Asp Thr Leu Pro Gly Tyr Glu Glu
 125 130 135 140
 gct ctt cac atg agt cgc ttc aca gta gcc atg tgc ggg cag aaa gca 542
 Ala Leu His Met Ser Arg Phe Thr Val Ala Met Cys Gly Gln Lys Ala
 145 150 155

177/307

cct gat cta ccc cca gta cct gaa gaa aag cag ctg cct cca aca gag 590
 Pro Asp Leu Pro Pro Val Pro Glu Glu Lys Gln Leu Pro Pro Thr Glu
 160 165 170
 aag gag tcg act cga ata gtt gac tct tgg aac tgatgag agctgtcatt 640
 Lys Glu Ser Thr Arg Ile Val Asp Ser Trp Asn
 175 180
 ttataaatag gaggaggatg atgtccagag tctgtgggaa aatggaacac atacttttct 700
 aaccctcaga agttttaaga tggcatctaa caccatcatt ctatgggaaa gatggttctt 760
 actcttcgtt cacaggcctt tatatcttcc gatacagaat gctctaattg ggaactctaa 820
 ttttgiatcc aatggccaaa atctgcaagt aatctctagc cacactgatt actactaaac 880
 caggaaagca tcaaggatc ttgaattcct ttaactattg agtgcataa gaattcctgt 940
 acccacatga tactgcaagt tgtgtctctc tctgtcagct aatccactgc ggtaactgg 1000
 aaaagaaga caacagtgc agcacagcca tcgacattaa tgcactgaat gcatgcatct 1060
 ttctctctga gacagcaatc gattttacac cgaatgaaa tgatcatctt agacagcaca 1120
 acataccac tcggatatct aaaagctagg gatggcattg ctgatatggg caaagagaac 1180
 acagtatagt atttaagtgc caaatatcag tctttctttc tctctggtcc taccctcag 1240
 cagtatgaaa aactccatac tgtgcagtc cagttggatt aattcttcag ttctctcgca 1300
 ctgcaaacac atatatgtgc gcacatgcat gtatactgc accctgtttt aactctaaag 1360
 gaatagtgtt gctttacttc tttctgttt tgcttgacc acttaagcc acaacacctc 1420
 tatagtaca cagctagtc tctagtgtg gccctcactg ccacctagag gagccatggt 1480
 ggaaaacaca ctctctcctt tgagcctatc tgcacatctc tcgagttctt ggagcaaaaa 1540
 ctaaatgctg aactaagcct gggtgagatg ctcccatgg accatgccgc agcacagtgc 1600
 taatctatcc aaaaaacata ccacctcca aagtattatt attggaaaat cgaggaagtg 1660
 acgcacattt agggaaaaac tactcacctt agaaaagtca ctgaaatcct tttttttttt 1720
 tttgagatgg agttttgtc ttgtagcca ggctgggatg caatggcatg gtctcagctc 1780

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actgtaacct ccacctcccg gattcaagca attcttctgc ctcagcttcc cgactagctg 1840
ggattacagc tgcccgccac cgtgcccagc taatttttgt atttttagtg gagagggggt 1900
ttcaccatgt tggccagtct ggtctagaac tcctgacgtc aggtgatccg cccaccttgg 1960
cctcccaaag tgctggaatt agaggcctga cccctgctc ctggcctgaa atctttaaag 2020
ccgttttttc cctaaaaaac gggaaataat aacacctcag aaggtttttg tgaagatcaa 2080
agaagctaaa tatatgtggc atgatttgta aagtgttatg catatgtatg ttattcttcc 2140
tactgtcttc taaccttccc ttgctgcta tgacttatct gagagccatg ttcccattta 2200
tctttttgcc aactatgta ctgttgctac acctgaaatg gctttgtttt tatcaataaa 2260
tacttgttga ttgtggtaaa cagc 2284

<210> 86

<211> 1737

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (236)... (1024)

<400> 86

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gccggcccca ggcggtgctt ctccccacca ccgccagct cagctcagcc cagcccagcc 120
cactctgccc ttagaggccc ttctcccaa agacgcactc cagaagtctc gcctcgtgc 180
ggctgaggag cctgggatcc cagacctgaa caagtgaac ccccgccct gaaga atg 238
Met
ggc aag acg ttt tcc cag ctg ggc tct tgg cgg gag gat gag aac aag. 286

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Gly Lys Thr Phe Ser Gln Leu Gly Ser Trp Arg Glu Asp Glu Asn Lys
 5 10 15
 tca atc ctg tcc tcc aaa cca gcc att ggc agc aag gct gtc aac tac 334
 Ser Ile Leu Ser Ser Lys Pro Ala Ile Gly Ser Lys Ala Val Asn Tyr
 20 25 30
 tcc agc acc ggt agc agc aag tct ttt tgt tcc tgt gtg cct tgt gaa 382
 Ser Ser Thr Gly Ser Ser Lys Ser Phe Cys Ser Cys Val Pro Cys Glu
 35 40 45
 gga act gct gat gcc agc ttc gtg act tgt ccc acc tgc cag ggc agt 430
 Gly Thr Ala Asp Ala Ser Phe Val Thr Cys Pro Thr Cys Gln Gly Ser
 50 55 60 65
 ggc aag att ccc caa gag ctg gag aag cag ttg gtg gct ctc att ccc 478
 Gly Lys Ile Pro Gln Glu Leu Glu Lys Gln Leu Val Ala Leu Ile Pro
 70 75 80
 tat ggg gac cag agg ctg aag ccc aag cac acg aag ctc ttt gtg ttc 526
 Tyr Gly Asp Gln Arg Leu Lys Pro Lys His Thr Lys Leu Phe Val Phe
 85 90 95
 ctg gcc gtg ctc atc tgc ctg gtg acc tcc tcc ttc atc gtc ttt ttc 574
 Leu Ala Val Leu Ile Cys Leu Val Thr Ser Ser Phe Ile Val Phe Phe
 100 105 110
 ctg ttt ccc cgg tcc gtc att gtg cag cct gca ggc ctc aac tcc tcc 622
 Leu Phe Pro Arg Ser Val Ile Val Gln Pro Ala Gly Leu Asn Ser Ser
 115 120 125
 aca gtg gcc ttt gat gag gct gat atc tac ctc aac ata acg aat atc 670
 Thr Val Ala Phe Asp Glu Ala Asp Ile Tyr Leu Asn Ile Thr Asn Ile

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130 135 140 145
 tta aac atc tcc aat ggc aac tac tac ccc att atg gtg aca cag ctg 718
 Leu Asn Ile Ser Asn Gly Asn Tyr Tyr Pro Ile Met Val Thr Gln Leu
 150 155 160
 acc ctc gag gtt ctg cac ctg tcc ctc gtg gtg ggg cag gtt tcc aac 766
 Thr Leu Glu Val Leu His Leu Ser Leu Val Val Gly Gln Val Ser Asn
 165 170 175
 aac ctt ctc cta cac att ggc cct ttg gcc agt gaa cag atg ttt tac 814
 Asn Leu Leu Leu His Ile Gly Pro Leu Ala Ser Glu Gln Met Phe Tyr
 180 185 190
 gca gta gct acc aag ata cgg gat gaa aac aca tac aaa atc tgt acc 862
 Ala Val Ala Thr Lys Ile Arg Asp Glu Asn Thr Tyr Lys Ile Cys Thr
 195 200 205
 tgg ctg gaa atc aaa gtc cac cat gtg ctt ttg cac atc cag ggc acc 910
 Trp Leu Glu Ile Lys Val His His Val Leu Leu His Ile Gln Gly Thr
 210 215 220 225
 ctg acc tgt tca tac ctg agc cat tca gag cag ctg gtc ttt cag agc 958
 Leu Thr Cys Ser Tyr Leu Ser His Ser Glu Gln Leu Val Phe Gln Ser
 230 235 240
 tat gaa tat gtg gac tgc cga gga aac gca tct gtg ccc cac cag ctg 1006
 Tyr Glu Tyr Val Asp Cys Arg Gly Asn Ala Ser Val Pro His Gln Leu
 245 250 255
 acc cct cac cca cca tgacctgtc tgctgtccct gtactccagg cacctgcaac 1060
 Thr Pro His Pro Pro
 260

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cctggtctat atctcccaca actccctggt gactaaggaa ggactacaga ggctttgcc 1120
aaggagaagc cctgectcat cacaccetta cctcccaccc cctcagcaca ggaagcttgc 1180
tttgaagtta acttcataca cacacactca tatectccag tttccccag attctttcag 1240
gggctgccat cagattctgc ccttggttag tttttgttt ttttttttg tagagacaga 1300
gtctcactgt tggccaggt tggtttgaa ctctgggct caagcgatcc tcccttcttg 1360
gcctcccaaa gcacttgat tacagatgtg agcctgtgcc tggctggtct ttcttgagga 1420
aaatctgacc tggcattttc ttgaggcacc ttagattccc tggagtggca cctggccttt 1480
ctgtactgag cacctggtca gtctgaaggg ggcatctcac cccagctcca tcagggttg 1540
cagtcctgtc tgaatgtgga gagagctgta gttttatctg gcttttaaaa catggacctg 1600
ccggctgggc gcagtggctt acacctgtaa tccagttact ttggggaggcc gaagtgggtg 1660
gatcattga gggcaggagt tcgtgaccag cctggtcaac atggtgaaac cttgtctcta 1720
ctaaaaatac aaaaatt 1737

<210> 87

<211> 1556

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)... (609)

<400> 87

agcgctcaact cgctcgcaact cagtcgcggg aggcttcccc gcgcgggccc cgtccccccc 60
gtccccggc accagaagtt cctctgcgcg tccgacggcg ac atg ggc gtc ccc. 114

Met Gly Val Pro

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acg gcc ctg gag gcc ggc agc tgg cgc tgg gga tcc ctg ctc ttc gct 162

Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly Ser Leu Leu Phe Ala

5 10 15 20

ctc ttc ctg gct gcg tcc cta ggc aaa gat gca cca tcc aac tgt gtg 210

Leu Phe Leu Ala Ala Ser Leu Gly Lys Asp Ala Pro Ser Asn Cys Val

25 30 35

gtg tac cca tcc tcc tcc cag gag agt gaa aac atc acg gct gca gcc 258

Val Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile Thr Ala Ala Ala

40 45 50

ctg gct acg ggt gcc tgc atc gta gga atc ctc tgc ctc ccc ctc atc 306

Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu Ile

55 60 65

ctg ctc ctg gtc tac aag caa agg cag gca gcc tcc aac cgc cgt gcc 354

Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg Arg Ala

70 75 80

cag gag ctg gtg cgg atg gac agc aac att caa ggg att gaa aac ccc 402

Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile Glu Asn Pro

85 90 95 100

ggc ttt gaa gcc tca cca cct gcc cag ggg ata ccc gag gcc aaa gtc 450

Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro Glu Ala Lys Val

105 110 115

agg cac ccc ctg tcc tat gtg gcc cag cgg cag cct tct gag tct ggg 498

Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro Ser Glu Ser Gly

120 125 130

cgg cat ctg ctt tcg gag ccc agc acc ccc ctg tct cct cca ggc ccc 546

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Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser Pro Pro Gly Pro

135

140

145

gga gac gtc ttc ttc cca tcc ctg gac cct gtc cct gac tct cca aac 594

Gly Asp Val Phe Phe Pro Ser Leu Asp Pro Val Pro Asp Ser Pro Asn

150

155

160

ttt gag gtc atc tagc ccagctgggg gacagtgggc tgttgtggct gggtctgggg 650

Phe Glu Val Ile

165

caggtgcatt tgagccaggg ctggctctgt gagtggcctc cttggcctcg gccctggttc 710

cctccctcct gctctgggct cagatactgt gacatcccag aagcccagcc cctcaacccc 770

tctggatgct acatggggat gctggacggc tcagcccctg ttccaaggat tttgggggtgc 830

tgagattctc ccctagagac ctgaaattca ccagctacag atgccaaatg acttacatct 890

taagaagtct cagaacgtcc agcccttcag cagctctcgt tctgagacat gagccttggg 950

atgtggcagc atcagtggga caagatggac actggggcac cctcccaggc accagacaca 1010

gggcacgggtg gagagacttc tccccgtgg cgccttggc tccccgttt tgcccagggc 1070

tgcctctctg tcagacttcc tctttgtacc acagtggctc tggggccagg cctgcctgcc 1130

cactggccat cgccaccttc ccagctgcc tcctaccagc agtttctctg aagatctgtc 1190

aacagggttaa gtcaatctgg ggcttccact gcctgcattc cagtcccag agcttgggtg 1250

tcccgaaacg ggaagtacat attggggcat ggtggcctcc gtgagcaaat ggtgtcttgg 1310

gcaatctgag gccaggacag atgttcccc acccactgga gatggtgctg agggaggtgg 1370

gtggggcctt ctgggaaggt gagtggagag gggcacctgc cccccgcct cccatcccc 1430

tactcccact gctcagcgcg ggccattgca agggtgccac acaatgtctt gtccaccctg 1490

ggacacttct gagtatgaag cgggatgcta ttaaaaacta catggggaaa caggtgcaaa 1550

ccctgg 1556

184/307

<210> 88

<211> 1855

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (222)... (953)

<400> 88

cagagatgga atttcaccgt gttgcctagg ctggtctgga gctcttgatc tcaagcgatc 60

ctccctgcct cggcctccca acgtgctggg attataggcg tgagccaccg ctccctggcca 120

gggtctgttc ctagttgcaa cagttcttgg aaaccacactc gagagggcca cgcctccatt 180

caccaggcca cgcatacaaa gaggcaaac caggagccaa c atg agc tcg ggg 233

Met Ser Ser Gly

1

act gaa ctg ctg tgg ccc gga gca gcg ctg ctg gtg ctg ttg ggg gtg 281

Thr Glu Leu Leu Trp Pro Gly Ala Ala Leu Leu Val Leu Leu Gly Val

5 10 15 20

gca gcc agt ctg tgt gtg cgc tgc tca cgc cca ggt gca aag agg tca 329

Ala Ala Ser Leu Cys Val Arg Cys Ser Arg Pro Gly Ala Lys Arg Ser

25 30 35

gag aaa atc tac cag cag aga agt ctg cgt gag gac caa cag agc ttt 377

Glu Lys Ile Tyr Gln Gln Arg Ser Leu Arg Glu Asp Gln Gln Ser Phe

40 45 50

acg ggg tcc cgg acc tac tcc ttg gtc ggg cag gca tgg cca gga ccc 425

Thr Gly Ser Arg Thr Tyr Ser Leu Val Gly Gln Ala Trp Pro Gly Pro

185/307

55	60	65	
ctg gcg gac atg gca ccc aca agg aag gac aag ctg ttg caa ttc tac			473
Leu Ala Asp Met Ala Pro Thr Arg Lys Asp Lys Leu Leu Gln Phe Tyr			
70	75	80	
ccc agc ctg gag gat cca gca tct tcc agg tac cag aac ttc agc aaa			521
Pro Ser Leu Glu Asp Pro Ala Ser Ser Arg Tyr Gln Asn Phe Ser Lys			
85	90	95	100
gga agc aga cac ggg tcg gag gaa gcc tac ata gac ccc att gcc atg			569
Gly Ser Arg His Gly Ser Glu Glu Ala Tyr Ile Asp Pro Ile Ala Met			
105	110	115	
gag tat tac aac tgg ggg cgg ttc tcg aag ccc cca gaa gat gat gat			617
Glu Tyr Tyr Asn Trp Gly Arg Phe Ser Lys Pro Pro Glu Asp Asp Asp			
120	125	130	
gcc aat tcc tac gag aat gtg ctc att tgc aag cag aaa acc aca gag			665
Ala Asn Ser Tyr Glu Asn Val Leu Ile Cys Lys Gln Lys Thr Thr Glu			
135	140	145	
aca ggt gcc cag cag gag ggc ata ggt ggc ctc tgc aga ggg gac ctc			713
Thr Gly Ala Gln Gln Glu Gly Ile Gly Gly Leu Cys Arg Gly Asp Leu			
150	155	160	
agc ctg tca ctg gcc ctg aag act ggc ccc act tct ggt ctc tgt ccc			761
Ser Leu Ser Leu Ala Leu Lys Thr Gly Pro Thr Ser Gly Leu Cys Pro			
165	170	175	180
tct gcc tcc ccg gaa gaa gat gag gaa tct gag gat tat cag aac tca			809
Ser Ala Ser Pro Glu Glu Asp Glu Glu Ser Glu Asp Tyr Gln Asn Ser			
185	190	195	

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gca tcc atc cat cag tgg cgc gag tcc agg aag gtc atg ggg caa ctc 857
 Ala Ser Ile His Gln Trp Arg Glu Ser Arg Lys Val Met Gly Gln Leu
 200 205 210
 cag aga gaa gca tcc cct ggc ccg gtg gga agc cca gac gag gag gac 905
 Gln Arg Glu Ala Ser Pro Gly Pro Val Gly Ser Pro Asp Glu Glu Asp
 215 220 225
 ggg gaa ccg gat tac gtg aat ggg gag gtg gca gcc aca gaa gcc 950
 Gly Glu Pro Asp Tyr Val Asn Gly Glu Val Ala Ala Thr Glu Ala
 230 235 240
 tagggcagac caagaagaaa ggagccaagg caaagaggga ccactgtgct catggaccca 1010
 tcgctgcctt ccaaggacca ttcccagag ctactcaact ttttaagcccc tgccatgggt 1070
 gctcctggaa ggagaaccag ccacctgag gaccacctgg ccatgcgtgc acagcctggg 1130
 aaaagacagt tactcacggg agctgcaggc ccgtcaccaa gccctctccc gaccagget 1190
 ttgtggggca ggcacctggt accaagggtg acccggtcc tggtatggac ggatgcgcag 1250
 gatttaggat aagctgtcac ccagtcacca taacaaaacc actgtccaac actggtatct 1310
 gtgttctttt gtgtatgaa ttggattcc taattgctat tgttggttgc tggggtttta 1370
 aatgattgat aagcttgtag agttaactta tagaggggga gccatattta acattctgga 1430
 ttccagagta gagatttctg tgttgtctcc tagaaagcat tacatgtagt ttatttcagc 1490
 atccttggtg ggtggggccc tggtctctct cccctttggt gggacctccc ctttctttgg 1550
 gcttcagttc actcaggaag aaatgagget gtcgccatct ttatgtgctt ccagtggaaa 1610
 tgtcacttgc tacagacaat agtgcagtag agtctagaga agtagtgacc agaacagggc 1670
 agagtaggtc cctccatgg cctgaatcc tctctgctc cagggtggc ctctgcagag 1730
 ctgattaaac agtgttgtag ctgtctcatg ggaagagctg gggcccagag ggaccttgag 1790
 tcagaaatgt tgccagaaaa agtatctcct ccaacaaaa catctcaata aaaccatttt 1850
 agttg 1855

187/307

<210> 89

<211> 2530

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (28)... (1314)

<400> 89

agcgcggcgg ggcgatgtgt gattacc atg gcg agg agt ctc tgt ccg ggg 51

Met Ala Arg Ser Leu Cys Pro Gly

1

5

gcc tgg cta agg aaa ccc tat tac ctc cag gct cgc ttc tca tat gtg 99

Ala Trp Leu Arg Lys Pro Tyr Tyr Leu Gln Ala Arg Phe Ser Tyr Val

10

15

20

cgg atg aaa tat ctt ttc ttt tcc tgg tta gtg gtt ttt gtt gga agc 147

Arg Met Lys Tyr Leu Phe Phe Ser Trp Leu Val Val Phe Val Gly Ser

25

30

35

40

tgg att ata tat gtg cag tat tct acc tat aca gaa tta tgc aga gga 195

Trp Ile Ile Tyr Val Gln Tyr Ser Thr Tyr Thr Glu Leu Cys Arg Gly

45

50

55

aag gac tgt aag aaa ata ata tgt gac aag tac aag act gga gtt att 243

Lys Asp Cys Lys Lys Ile Ile Cys Asp Lys Tyr Lys Thr Gly Val Ile

60

65

70

gat ggg cct gca tgt aac agc ctt tgt gtt aca gaa act ctt tac ttt 291

188/307

Asp Gly Pro Ala Cys Asn Ser Leu Cys Val Thr Glu Thr Leu Tyr Phe
 75 80 85
 gga aaa tgt tta tcc acc aag ccc aac aat cag atg tat tta ggg att 339
 Gly Lys Cys Leu Ser Thr Lys Pro Asn Asn Gln Met Tyr Leu Gly Ile
 90 95 100
 tgg gat aat cta cca ggt gtt gtg aaa tgt caa atg gaa caa gcg ctt 387
 Trp Asp Asn Leu Pro Gly Val Val Lys Cys Gln Met Glu Gln Ala Leu
 105 110 115 120
 cat ctt gat ttt gga act gaa ttg gaa cca aga aaa gaa ata gtg cta 435
 His Leu Asp Phe Gly Thr Glu Leu Glu Pro Arg Lys Glu Ile Val Leu
 125 130 135
 ttt gat aag cca act aga gga act act gta caa aaa ttt aaa gaa atg 483
 Phe Asp Lys Pro Thr Arg Gly Thr Thr Val Gln Lys Phe Lys Glu Met
 140 145 150
 gtc tat agt ctc ttt aag gca aaa ttg ggt gac caa gga aac ctc tct 531
 Val Tyr Ser Leu Phe Lys Ala Lys Leu Gly Asp Gln Gly Asn Leu Ser
 155 160 165
 gaa ctg gtt aat ctc atc ttg acg gtg gct gat gga gac aaa gat ggc 579
 Glu Leu Val Asn Leu Ile Leu Thr Val Ala Asp Gly Asp Lys Asp Gly
 170 175 180 200
 cag gtt tcc ttg gga gaa gca aag tcg gca tgg gca ctt ctt caa ctg 627
 Gln Val Ser Leu Gly Glu Ala Lys Ser Ala Trp Ala Leu Leu Gln Leu
 185 190 195 200
 aat gaa ttt ctt ctc atg gtg ata ctt caa gat aaa gaa cat acc ccc 675
 Asn Glu Phe Leu Leu Met Val Ile Leu Gln Asp Lys Glu His Thr Pro

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205	210	215	
aaa tta atg gga ttc tgt ggt gac ctc tat gtg atg gaa agt gtt gaa			723
Lys Leu Met Gly Phe Cys Gly Asp Leu Tyr Val Met Glu Ser Val Glu			
220	225	230	
tat acc tct ctt tat gga ata agc ctt cct tgg gtc att gaa ctt ttt			771
Tyr Thr Ser Leu Tyr Gly Ile Ser Leu Pro Trp Val Ile Glu Leu Phe			
235	240	245	
att cca tct ggg ttc aga aga agc atg gat cag ctg ttc aca cca tca			819
Ile Pro Ser Gly Phe Arg Arg Ser Met Asp Gln Leu Phe Thr Pro Ser			
250	255	260	
tgg cca aga aag gcc aaa ata gcc ata gga ctt cta gaa ttt gtg gaa			867
Trp Pro Arg Lys Ala Lys Ile Ala Ile Gly Leu Leu Glu Phe Val Glu			
265	270	275	280
gat gtt ttc cat ggc ccc tac gga aat ttc ctc atg tgc gat act agt			915
Asp Val Phe His Gly Pro Tyr Gly Asn Phe Leu Met Cys Asp Thr Ser			
285	290	295	
gcc aaa aac cta gga tat aat gat aag tat gat ttg aaa atg gtg gat			963
Ala Lys Asn Leu Gly Tyr Asn Asp Lys Tyr Asp Leu Lys Met Val Asp			
300	305	310	
atg aga aaa att gtg cca gag aca aac ctg aaa gaa ctt att aag gat			1011
Met Arg Lys Ile Val Pro Glu Thr Asn Leu Lys Glu Leu Ile Lys Asp			
315	320	325	
cgt cac tgt gag tct gat ttg gac tgt gtc tat ggc aca gat tgt aga			1059
Arg His Cys Glu Ser Asp Leu Asp Cys Val Tyr Gly Thr Asp Cys Arg			
330	335	340	

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act agc tgt gat cag agt aca atg aag tgt act tca gaa gtg ata caa 1107

Thr Ser Cys Asp Gln Ser Thr Met Lys Cys Thr Ser Glu Val Ile Gln

345 350 355 360

cca aac ttg gca aaa gct tgt cag tta ctc aaa gac tac cta ctg cgt 1155

Pro Asn Leu Ala Lys Ala Cys Gln Leu Leu Lys Asp Tyr Leu Leu Arg

365 370 375

ggc gct cca agt gaa att cgt gaa gaa tta gaa aag cag ctt tat tct 1203

Gly Ala Pro Ser Glu Ile Arg Glu Glu Leu Glu Lys Gln Leu Tyr Ser

380 385 390

tgt att gct ctc aaa gtc aca gca aat caa atg gaa atg gaa cat tct 1251

Cys Ile Ala Leu Lys Val Thr Ala Asn Gln Met Glu Met Glu His Ser

395 400 405

ttg ata cta aat aac cta aaa aca tta ttg tgg aag aaa att tcc tac 1299

Leu Ile Leu Asn Asn Leu Lys Thr Leu Leu Trp Lys Lys Ile Ser Tyr

410 415 420

act aat gac tct tagttcatt tggacataat taccatttta agaaacctgc 1350

Thr Asn Asp Ser

425

cacttttaaa gaacaatttt gagcattaaa aaaaaatggc ttcaaattcc tgccagttac 1410

acaaaactcc ttccccccag gctgagaag ccatcagtat gtgattactg aagtaatggc 1470

aggtgtagga tcaacaggtc cccaagatgt cattcctgcc cttttagaag cctgtttaca 1530

tctccgaagt acattcattg tgtaactatt ttgactgact ttaaaaacca atgctgtgaa 1590

aagcttcatt ccataaacat caacagtgag tgattttag atttacctta gccaaaatac 1650

caatgctgga agcatttgtt ttgcattgaa gctgctgttc aacaagaaaa ttataaatt 1710

tactaatgtc ttagcatggt aaagtttgca cattaacaga aattaagact gcaaagcagg 1770

191/307

ttaaacttgc ttctttataa aacagatggt gggttaatag catggtttac tgtattaaag 1830
 acttatacac ccatttttaa cctcattcag acatcaaggt atgtgtagct tcacaatggt 1890
 tcaagtggct tacttcaaga aatcttatac ttgacagtac accaatttta ttgactaaaa 1950
 atggatgaac tttcctaaag attcaaaggg cccatcttag tatcacgcag ctgactgagc 2010
 ccttcaaaac tgacatctta aggcccaatc aagatccaca tatectgatt ttgaactatg 2070
 tgaaagtggg actgttaagt gcaagactaa aataaattat agcagacttt ttagtaataa 2130
 ctttcatttt tcaaacagta tatectgtgg gccaaagggc tatttcttaa agaggcatgt 2190
 aaatgtattt atttatctaa tgtttttttc cccatgtaaa ctgatatac aaggtttagt 2250
 atttgcctct ctttcatatt attttcacac gtatactcag atttggcatg tacctttcaa 2310
 catctccata aaattaaaca ccttttgagg aaaagatcca ctattttctg ctcaaaggtt 2370
 tcgcctacct aaagtgaac atgttaaaaa tctatgtgac catcactgga cagctttctc 2430
 tcaaaacttt ctttcaacgc catggattag caccagtttt gtttacttta aggtactttt 2490
 cccattcatc atctggttat aataaatgga tggaagaaat 2530

<210> 90

<211> 1911

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232)... (1083)

<400> 90

aaaatatgag acggggaatc atcgtgtgat gtgtgtgctg cctttggctg agtgtgtgga 60
 gtcttgctca ggtgttaggt acagtgtgtt tgatcgtggt ggcttgaggg gaacccgctg 120
 ttcagagctg tgactgcggc tgcactcaga gaagctgccc ttggctgctc gtagcgccgg 180

192/307

gccttctctc ctcgtcatca tccagagcag ccagtgccg ggaggcagaa g atg ccc 237
Met Pro

cac tcc agc ctg cat cca tcc atc ccg tgt ccc agg ggt cac ggg gcc 285
His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His Gly Ala

5 10 15

cag aag gca gcc ttg gtt ctg ctg agt gcc tgc ctg gtg acc ctt tgg 333
Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr Leu Trp

20 25 30

ggg cta gga gag cca cca gag cac act ctc egg tac ctg gtg ctc cac 381
Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val Leu His

35 40 45 50

cta gcc tcc ctg cag ctg gga ctg ctg tta aac ggg gtc tgc agc ctg 429
Leu Ala Ser Leu Gln Leu Gly Leu Leu Leu Asn Gly Val Cys Ser Leu

55 60 65

gct gag gag ctg cac cac atc cac tcc agg tac cgg ggc agc tac tgg 477
Ala Glu Glu Leu His His Ile His Ser Arg Tyr Arg Gly Ser Tyr Trp

70 75 80

agg act gtg cgg gcc tgc ctg ggc tgc ccc ctc cgc cgt ggg gcc ctg 525
Arg Thr Val Arg Ala Cys Leu Gly Cys Pro Leu Arg Arg Gly Ala Leu

85 90 95

ttg ctg ctg tcc atc tat ttc tac tac tcc ctc cca aat gcg gtc ggc 573
Leu Leu Leu Ser Ile Tyr Phe Tyr Tyr Ser Leu Pro Asn Ala Val Gly

100 105 110

ccg ccc ttc act tgg atg ctt gcc ctc ctg ggc ctc tcg cag gca ctg 621

193/307

Pro Pro Phe Thr Trp Met Leu Ala Leu Leu Gly Leu Ser Gln Ala Leu
 115 120 125 130
 aac atc ctc ctg ggc ctc aag ggc ctg gcc cca gct gag atc tct gca 669
 Asn Ile Leu Leu Gly Leu Lys Gly Leu Ala Pro Ala Glu Ile Ser Ala
 135 140 145
 gtg tgt gaa aaa ggg aat ttc aac gtg gcc cat ggg ctg gca tgg tca 717
 Val Cys Glu Lys Gly Asn Phe Asn Val Ala His Gly Leu Ala Trp Ser
 150 155 160
 tat tac atc gga tat ctg cgg ctg atc ctg cca gag ctc cag gcc cgg 765
 Tyr Tyr Ile Gly Tyr Leu Arg Leu Ile Leu Pro Glu Leu Gln Ala Arg
 165 170 175
 att cga act tac aat cag cat tac aac aac ctg cta cgg ggt gca gtg 813
 Ile Arg Thr Tyr Asn Gln His Tyr Asn Asn Leu Leu Arg Gly Ala Val
 180 185 190
 agc cag cgg ctg tat att ctc ctc cca ttg gac tgt ggg gtg cct gat 861
 Ser Gln Arg Leu Tyr Ile Leu Leu Pro Leu Asp Cys Gly Val Pro Asp
 195 200 205 210
 aac ctg agt atg gct gac ccc aac att cgc ttc ctg gat aaa ctg ccc 909
 Asn Leu Ser Met Ala Asp Pro Asn Ile Arg Phe Leu Asp Lys Leu Pro
 215 220 225
 cag cag acc gct gac cgt gct ggc atc aag gat cgg gtt tac agc aac 957
 Gln Gln Thr Ala Asp Arg Ala Gly Ile Lys Asp Arg Val Tyr Ser Asn
 230 235 240
 agc atc tat gag ctt ctg gag aac ggg cag cgg aac ctg cag atg aca 1005
 Ser Ile Tyr Glu Leu Leu Glu Asn Gly Gln Arg Asn Leu Gln Met Thr

194/307

245 250 255
gca gct tct cgc tgt ccc agg agg ttc tcc ggc acc tgc ggc agg agg 1053
Ala Ala Ser Arg Cys Pro Arg Arg Phe Ser Gly Thr Cys Gly Arg Arg
260 265 270
aaa agg aag agg tta ctg tgg gca gct tgaagacctc agcgggtgcc 1100
Lys Arg Lys Arg Leu Leu Trp Ala Ala
275 280
agtacctcca cgatgtccca agagcctgag ctctcatca gtggaatgga aaagcccctc 1160
ctctctccga cggatttctc ttgagacctc gggtcaccag gccagagcct ccagtgggtct 1220
ccaagcctct ggactggggg ctctcttcag tggtgaatg tccagcagag ctatttcctt 1280
ccacaggggg ccttgcaggg aagggtccag gacttgacat ctttaagatgc gtcttgtccc 1340
cttgggccag tcatttcccc tctctgagcc tcggtgtctt caacctgtga aatgggatca 1400
taatcactgc cttacctccc tcacggttgt tgtgaggact gagtgtgtgg aagtttttca 1460
taaactttgg atgctagtgt acttaggggg tgtgccaggt gtctttcatg gggccttcca 1520
gacctactcc ccaccttct ccccttcctt tgcccgggga cgccgaactc tctcaatggt 1580
atcaacaggc tccttgcgcc tctggtcct ggtcatgttc cattattggg gagccccagc 1640
agaagaatgg agaggaggag gaggtgagt ttgggtatt gaatcccccg gctcccaccc 1700
tgcagcatca aggttgcata ggactctcct gccgggcaac tcttgcgtaa tcatgactat 1760
ctctaggatt ctggcaccac ttcttccct ggcctttaa gcctagctgt gtatcgcac 1820
ccccaccca ctagagtact cctctcact tgcggtttcc ttatactcca cccctttctc 1880
aacggtcctt ttttaaagca catctcagat t 1911

<210> 91

<211> 476

<212> PRT

195/307

<213> Homo sapiens

<400> 91

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met

1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser

20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr

35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly

50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65 70 75 80

Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln

85 90 95

Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro

100 105 110

Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val

115 120 125

Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr

130 135 140

Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser

145 150 155 160

Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala

165 170 175

Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu

196/307

180 185 190
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
195 200 205
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
210 215 220
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser
225 230 235 240
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile
245 250 255
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His
260 265 270
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu
275 280 285
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr
290 295 300
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys
305 310 315 320
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro
325 330 335
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly
340 345 350
Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
355 360 365
Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
370 375 380

197/307

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu His Ser Leu

385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys

405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile

420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His

435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg

450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly

465 470 475

<210> 92

<211> 226

<212> PRT

<213> Homo sapiens

<400> 92

Met Ser Arg Ala Gln Ile Trp Ala Leu Val Ser Gly Val Gly Gly Phe

1 5 10 15

Gly Ala Leu Val Ala Ala Thr Thr Ser Asn Glu Trp Lys Val Thr Thr

20 25 30

Arg Ala Ser Ser Val Ile Thr Ala Thr Trp Val Tyr Gln Gly Leu Trp

35 40 45

Met Asn Cys Ala Gly Asn Ala Leu Gly Ser Phe His Cys Arg Pro His

198/307

50 55 60
Phe Thr Ile Phe Lys Val Ala Gly Tyr Ile Gln Ala Cys Arg Gly Leu
65 70 75 80
Met Ile Ala Ala Val Ser Leu Gly Phe Phe Gly Ser Ile Phe Ala Leu
85 90 95
Phe Gly Met Lys Cys Thr Lys Val Gly Gly Ser Asp Lys Ala Lys Ala
100 105 110
Lys Ile Ala Cys Leu Ala Gly Ile Val Phe Ile Leu Ser Gly Leu Cys
115 120 125
Ser Met Thr Gly Cys Ser Leu Tyr Ala Asn Lys Ile Thr Thr Glu Phe
130 135 140
Phe Asp Pro Leu Phe Val Glu Gln Lys Tyr Glu Leu Gly Ala Ala Leu
145 150 155 160
Phe Ile Gly Trp Ala Gly Ala Ser Leu Cys Ile Ile Gly Gly Val Ile
165 170 175
Phe Cys Phe Ser Ile Ser Asp Asn Asn Lys Thr Pro Arg Tyr Thr Tyr
180 185 190
Asn Gly Ala Thr Ser Val Met Ser Ser Arg Thr Lys Tyr His Gly Gly
195 200 205
Glu Asp Phe Lys Thr Thr Asn Pro Ser Lys Gln Phe Asp Lys Asn Ala
210 215 220
Tyr Val
225

<210> 93

199/307

<211> 305

<212> PRT

<213> Homo sapiens

<400> 93

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly

1 5 10 15

Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg

20 25 30

Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu

35 40 45

Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe

50 55 60

Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly

65 70 75 80

Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg

85 90 95

Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu

100 105 110

Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly

115 120 125

Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val

130 135 140

Glu Phe Arg Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His

145 150 155 160

Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala

200/307

165 170 175
Lys Lys Leu Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu
180 185 190
Gln Leu Ile Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys
195 200 205
Phe Leu Leu Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu
210 215 220
Asp Leu Glu Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp
225 230 235 240
Phe Thr Leu Asp His Pro Pro Lys Asp Trp Ala Tyr Ser Lys Gly Phe
245 250 255
Val Thr Ala Asp Met Ile Arg Glu His Leu Pro Ala Pro Gly Asp Asp
260 265 270
Val Leu Val Leu Leu Cys Gly Pro Pro Pro Met Val Gln Leu Ala Cys
275 280 285
His Pro Asn Leu Asp Lys Leu Gly Tyr Ser Gln Lys Met Arg Phe Thr
290 295 300
Tyr
305

<210> 94

<211> 227

<212> PRT

<213> Homo sapiens

<400> 94

201/307

Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
1 5 10 15
Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
20 25 30
Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
35 40 45
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
50 55 60
Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
65 70 75 80
Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
85 90 95
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
100 105 110
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
115 120 125
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
130 135 140
Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys
145 150 155 160
Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
165 170 175
Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
180 185 190
Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala

202/307

195 200 205
Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
210 215 220
Ala Ala Cys
225

<210> 95

<211> 441

<212> PRT

<213> Homo sapiens

<400> 95

Met Ala Ile His Lys Ala Leu Val Met Cys Leu Gly Leu Pro Leu Phe

1 5 10 15

Leu Phe Pro Gly Ala Trp Ala Gln Gly His Val Pro Pro Gly Cys Ser

20 25 30

Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu Cys Asp Arg Ser Gly Ala

35 40 45

Trp Gly Ile Val Leu Glu Ala Val Ala Gly Ala Gly Ile Val Thr Thr

50 55 60

Phe Val Leu Thr Ile Ile Leu Val Ala Ser Leu Pro Phe Val Gln Asp

65 70 75 80

Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln Val Phe Phe Leu Leu Gly

85 90 95

Thr Leu Gly Leu Phe Cys Leu Val Phe Ala Cys Val Val Lys Pro Asp

100 105 110

203/307

Phe Ser Thr Cys Ala Ser Arg Arg Phe Leu Phe Gly Val Leu Phe Ala
115 120 125
Ile Cys Phe Ser Cys Leu Ala Ala His Val Phe Ala Leu Asn Phe Leu
130 135 140
Ala Arg Lys Asn His Gly Pro Arg Gly Trp Val Ile Phe Thr Val Ala
145 150 155 160
Leu Leu Leu Thr Leu Val Glu Val Ile Ile Asn Thr Glu Trp Leu Ile
165 170 175
Ile Thr Leu Val Arg Gly Ser Gly Glu Gly Gly Pro Gln Gly Asn Ser
180 185 190
Ser Ala Gly Trp Ala Val Ala Ser Pro Cys Ala Ile Ala Asn Met Asp
195 200 205
Phe Val Met Ala Leu Ile Tyr Val Met Leu Leu Leu Leu Gly Ala Phe
210 215 220
Leu Gly Ala Trp Pro Ala Leu Cys Gly Arg Tyr Lys Arg Trp Arg Lys
225 230 235 240
His Gly Val Phe Val Leu Leu Thr Thr Ala Thr Ser Val Ala Ile Trp
245 250 255
Val Val Trp Ile Val Met Tyr Thr Tyr Gly Asn Lys Gln His Asn Ser
260 265 270
Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile Ala Leu Ala Ala Asn Ala
275 280 285
Trp Ala Phe Val Leu Phe Tyr Val Ile Pro Glu Val Ser Gln Val Thr
290 295 300
Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly Asp Met Tyr Pro Thr Arg

204/307

305 310 315 320

Gly Val Gly Tyr Glu Thr Ile Leu Lys Glu Gln Lys Gly Gln Ser Met

325 330 335

Phe Val Glu Asn Lys Ala Phe Ser Met Asp Glu Pro Val Ala Ala Lys

340 345 350

Arg Pro Val Ser Pro Tyr Ser Gly Tyr Asn Gly Gln Leu Leu Thr Ser

355 360 365

Val Tyr Gln Pro Thr Glu Met Ala Leu Met His Lys Val Pro Ser Glu

370 375 380

Gly Ala Tyr Asp Ile Ile Leu Pro Arg Ala Thr Ala Asn Ser Gln Val

385 390 395 400

Met Gly Ser Ala Asn Ser Thr Leu Arg Ala Glu Asp Met Tyr Ser Ala

405 410 415

Gln Ser His Gln Ala Ala Thr Pro Pro Lys Asp Gly Lys Asn Ser Gln

420 425 430

Val Phe Arg Asn Pro Tyr Val Trp Asp

435 440

<210> 96

<211> 265

<212> PRT

<213> Homo sapiens

<400> 96

Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys

1 5 10 15

205/307

Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro

20

25

30

Leu Val Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val

35

40

45

Ser Arg Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser

50

55

60

Thr Pro Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser

65

70

75

80

Ile Ser Gln Ile Ser Thr Thr Leu Pro Pro Thr Thr Ser Thr Lys Lys

85

90

95

Ser Gly Gly Ala Ser Val Val Pro His Pro Ser Pro Thr Pro Leu Ser

100

105

110

Gln Glu Glu Ala Asp Asn Asn Glu Asp Pro Ser Ile Glu Glu Glu Asp

115

120

125

Leu Leu Met Leu Asn Ser Ser Pro Ser Thr Ala Lys Asp Thr Leu Asp

130

135

140

Asn Gly Asp Tyr Gly Glu Pro Asp Tyr Asp Trp Thr Thr Gly Pro Arg

145

150

155

160

Asp Asp Asp Glu Ser Asp Asp Thr Leu Glu Glu Asn Arg Gly Tyr Met

165

170

175

Glu Ile Glu Gln Ser Val Lys Ser Phe Lys Met Pro Ser Ser Asn Ile

180

185

190

Glu Glu Glu Asp Ser His Phe Phe Phe His Leu Ile Ile Phe Ala Phe

195

200

205

Cys Ile Ala Val Val Tyr Ile Thr Tyr His Asn Lys Arg Lys Ile Phe

210 215 220

225 230 235 240

245 250 255

260 265

<211> 208

<212> PRT

<213> Homo sapiens

<400> 97

Met Leu Gly Leu Leu Val Ala Leu Leu Ala Leu Gly Leu Ala Val Phe

1 5 10 15

Ala Leu Leu Asp Val Trp Tyr Leu Val Arg Leu Pro Cys Ala Val Leu

20 25 30

Arg Ala Arg Leu Leu Gln Pro Arg Val Arg Asp Leu Leu Ala Glu Gln

35 40 45

Arg Phe Pro Gly Arg Val Leu Pro Ser Asp Leu Asp Leu Leu Leu His

50 55 60

Met Asn Asn Ala Arg Tyr Leu Arg Glu Ala Asp Phe Ala Arg Val Ala

65 70 75 80

His Leu Thr Arg Cys Gly Val Leu Gly Ala Leu Arg Glu Leu Arg Ala

85 90 95

207/307

His Thr Val Leu Ala Ala Ser Cys Ala Arg His Arg Arg Ser Leu Arg

100

105

110

Leu Leu Glu Pro Phe Glu Val Arg Thr Arg Leu Leu Gly Trp Asp Asp

115

120

125

Arg Ala Phe Tyr Leu Glu Ala Arg Phe Val Ser Leu Arg Asp Gly Phe

130

135

140

Val Cys Ala Leu Leu Arg Phe Arg Gln His Leu Leu Gly Thr Ser Pro

145

150

155

160

Glu Arg Val Val Gln His Leu Cys Gln Arg Arg Val Glu Pro Pro Glu

165

170

175

Leu Pro Ala Asp Leu Gln His Trp Ile Ser Tyr Asn Glu Ala Ser Ser

180

185

190

Gln Leu Leu Arg Met Glu Ser Gly Leu Ser Asp Val Thr Lys Asp Gln

195

200

205

<210> 98

<211> 400

<212> PRT

<213> Homo sapiens

<400> 98

Met Ala Trp Arg Arg Arg Glu Ala Ser Val Gly Ala Arg Gly Val Leu

1

5

10

15

Ala Leu Ala Leu Leu Ala Leu Ala Leu Cys Val Pro Gly Ala Arg Gly

20

25

30

Arg Ala Leu Glu Trp Phe Ser Ala Val Val Asn Ile Glu Tyr Val Asp

208/307

35 40 45
Pro Gln Thr Asn Leu Thr Val Trp Ser Val Ser Glu Ser Gly Arg Phe
50 55 60
Gly Asp Ser Ser Pro Lys Glu Gly Ala His Gly Leu Val Gly Val Pro
65 70 75 80
Trp Ala Pro Gly Gly Asp Leu Glu Gly Cys Ala Pro Asp Thr Arg Phe
85 90 95
Phe Val Pro Glu Pro Gly Gly Arg Gly Ala Ala Pro Trp Val Ala Leu
100 105 110
Val Ala Arg Gly Gly Cys Thr Phe Lys Asp Lys Val Leu Val Ala Ala
115 120 125
Arg Arg Asn Ala Ser Ala Val Val Leu Tyr Asn Glu Glu Arg Tyr Gly
130 135 140
Asn Ile Thr Leu Pro Met Ser His Ala Gly Thr Gly Asn Ile Val Val
145 150 155 160
Ile Met Ile Ser Tyr Pro Lys Gly Arg Glu Ile Leu Glu Leu Val Gln
165 170 175
Lys Gly Ile Pro Val Thr Met Thr Ile Gly Val Gly Thr Arg His Val
180 185 190
Gln Glu Phe Ile Ser Gly Gln Ser Val Val Phe Val Ala Ile Ala Phe
195 200 205
Ile Thr Met Met Ile Ile Ser Leu Ala Trp Leu Ile Phe Tyr Tyr Ile
210 215 220
Gln Arg Phe Leu Tyr Thr Gly Ser Gln Ile Gly Ser Gln Ser His Arg
225 230 235 240

209/307

Lys Glu Thr Lys Lys Val Ile Gly Gln Leu Leu Leu His Thr Val Lys

245

250

255

His Gly Glu Lys Gly Ile Asp Val Asp Ala Glu Asn Cys Ala Val Cys

260

265

270

Ile Glu Asn Phe Lys Val Lys Asp Ile Ile Arg Ile Leu Pro Cys Lys

275

280

285

His Ile Phe His Arg Ile Cys Ile Asp Pro Trp Leu Leu Asp His Arg

290

295

300

Thr Cys Pro Met Cys Lys Leu Asp Val Ile Lys Ala Leu Gly Tyr Trp

305

310

315

320

Gly Glu Pro Gly Asp Val Gln Glu Met Pro Ala Pro Glu Ser Pro Pro

325

330

335

Gly Arg Asp Pro Ala Ala Asn Leu Ser Leu Ala Leu Pro Asp Asp Asp

340

345

350

Gly Ser Asp Glu Ser Ser Pro Pro Ser Ala Ser Pro Ala Glu Ser Glu

355

360

365

Pro Gln Cys Asp Pro Ser Phe Lys Gly Asp Ala Gly Glu Asn Thr Ala

370

375

380

Leu Leu Glu Ala Gly Arg Ser Asp Ser Arg His Gly Gly Pro Ile Ser

385

390

395

400

<210> 99

<211> 192

<212> PRT

<213> Homo sapiens

210/307

<400> 99

Met Phe Cys Pro Leu Lys Leu Ile Leu Leu Pro Val Leu Leu Asp Tyr

1 5 10 15

Ser Leu Gly Leu Asn Asp Leu Asn Val Ser Pro Pro Glu Leu Thr Val

20 25 30

His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln Ser Thr Glu

35 40 45

Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu His

50 55 60

Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val Pro

65 70 75 80

Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Asn Leu Cys

85 90 95

Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln Gly

100 105 110

Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe Lys

115 120 125

Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Glu Leu Met

130 135 140

Val His Val Gly Gly Leu Ile Gln Met Gly Cys Val Phe Gln Ser Thr

145 150 155 160

Glu Val Lys His Val Thr Lys Val Glu Trp Ile Phe Ser Gly Arg Arg

165 170 175

Ala Lys Val Thr Arg Arg Lys His His Cys Val Arg Glu Gly Ser Gly

180 185 190

211/307

<210> 100

<211> 260

<212> PRT

<213> Homo sapiens

<400> 100

Met Ala Gly Ser Pro Leu Leu Trp Gly Pro Arg Ala Gly Gly Val Gly

1 5 10 15

Leu Leu Val Leu Leu Leu Gly Leu Phe Arg Pro Pro Pro Ala Leu

20 25 30

Cys Ala Arg Pro Val Lys Glu Pro Arg Gly Leu Ser Ala Ala Ser Pro

35 40 45

Pro Leu Ala Glu Thr Gly Ala Pro Arg Arg Phe Arg Arg Ser Val Pro

50 55 60

Arg Gly Glu Ala Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala

65 70 75 80

His Leu Leu Glu Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln

85 90 95

Glu Ala Glu Asp Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Val

100 105 110

Trp Gly Ala Pro Arg Asn Ser Asp Pro Ala Leu Gly Leu Asp Asp Asp

115 120 125

Pro Asp Ala Pro Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg

130 135 140

Leu Asp Pro Ala Ala Leu Ala Ala Gln Leu Val Pro Ala Pro Val Pro

145 150 155 160

Ala Ala Ala Leu Arg Pro Arg Pro Pro Val Tyr Asp Asp Gly Pro Ala

 165 170 175

Gly Pro Asp Ala Glu Glu Ala Gly Asp Glu Thr Pro Asp Val Asp Pro

 180 185 190

Glu Leu Leu Arg Tyr Leu Leu Gly Arg Ile Leu Ala Gly Ser Ala Asp

 195 200 205

Ser Glu Gly Val Ala Ala Pro Arg Arg Leu Arg Arg Ala Ala Asp His

 210 215 220

Asp Val Gly Ser Glu Leu Pro Pro Glu Gly Val Leu Gly Ala Leu Leu

225 230 235 240

Arg Val Lys Arg Leu Glu Thr Pro Ala Pro Gln Val Pro Ala Arg Arg

 245 250 255

Leu Leu Pro Pro

 260

<210> 101
<211> 1428
<212> DNA
<213> Homo sapiens
<400> 101

atggttgggtg ccatgtggaa ggtgattgtt tcgctgggtcc tgttgatgcc tggccccctgt	60
gatgggctgt ttcgtccct atacagaagt gtttccatgc cacctaaggg agactcagga	120
cagccatttat ttctcaccct ttacattgaa gctgggaaga tccaaaaagg aagagaattg	180
agtttgggtcg gccctttccc aggactgaac atgaagagtt atgccggctt cctcaccgtg	240

213/307

aataagactt acaacagcaa cctcttcttc tggttcttcc cagctcagat acagccagaa 300
gatgccccag tagttctctg gctacagggt gggccgggag gttcatccat gtttggaactc 360
tttgtggaac atgggcctta tgttgtcaca agtaacatga ccttgcgatga cagagacttc 420
ccctggacca caacgctctc catgctttac attgacaatc cagtgggcac aggcttcagt 480
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aaccctgtga gagaggtgaa gatcaacctg aacggaattg ctattggaga tggatatctt 720
gatcccgaat caattatagg gggctatgca gaattcctgt accaaattgg ctigtgtgat 780
gagaagcaaa aaaaglactt ccagaagcag tgccatgaat gcatagaaca catcaggaag 840
cagaactggg ttgaggectt tgaaatactg gataaactac tagatggcga ctaacaagt 900
gatccttcct acttccagaa tgttacagga tgtagtaatt actataactt tttgcgggtgc 960
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gaagatacag tacagtcagt taagccatgg ttaactgaaa tcatgaataa ttataaggtt 1140
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atgggcatgg actggaaagg atcccaggaa tacaagaagg cagaaaaaaaa agtttggaag 1260
atctttaaat ctgacagtga agtggttgtt tacatccggc aagcgggtga ctccatcag 1320
gtaattattc gaggtggagg acatatttta ccctatgacc agcctctgag agcttttgac 1380
atgattaatc gattcattta tggaaaagga tgggatcctt atgttgga 1428

<210> 102

<211> 678

<212> DNA

<213> Homo sapiens

214/307

<400> 102

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gctgctacca cgtccaatga gtggaaagt accacgcgag cctcctcggt gataacagcc 120
acttgggttt accagggtct gtggatgaac tgcgcaggta acgcgttggg ttctttccat 180
tgccgaccgc attttactat cttcaaagta gcaggttata tacaggcatg tagaggactt 240
atgategctg ctgtcagcct gggtctcttt ggttccatat ttgcgctctt tggaatgaag 300
tgtaccaaag tggagggtc cgataaagcc aaagctaaaa ttgcttggtt ggctgggatt 360
gtattcatac tgtcagggtc gtgtcaatg actggatggt ccctatatgc aaacaaaac 420
acaacggaat tctttgatcc tctcttgggt gagcaaaagt atgaattagg agccgctctg 480
tttattggat gggcaggagc ctactgtgc ataattgggt gtgtcatatt ttgcttttca 540
atatctgaca acaacaaaac acccagatac acatacaacg gggccacatc tgtcatgtct 600
tctcgacaa agtatcatgg tggagaagat tttaaaaca caaaccttc aaaacagttt 660
gataaaaatg ctatgtc 678

<210> 103

<211> 915

<212> DNA

<213> Homo sapiens

<400> 103

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ctggccctgg ctgtgggtc ctacttgggt cggagggtccc gccggcctca ggtaactctc 120
ctggacccca atgaaaagta cctgctacga ctgctagaca agacgactgt gagccacaac 180
accaagaggt tccgttggc cctgccacc gccaccaca ccttggggct gcctgtgggc 240
aaacatatct acctctccac ccgaattgat ggcagcctgg tcatcaggcc atacacacct 300
gtcaccagtg atgaggatca aggctatgtg gatcttgtca tcaaggctca cctgaagggt 360

215/307

gtgcacccca aatttcctga gggaggggaag atgtctcagt acctggatag cctgaaggtt 420
 ggggatgttg tggagtttcg ggggccaagc gggttgctca cttacactgg aaaagggcat 480
 tttaacattc agcccaacaa gaaatctcca ccagaacccc gagtggcgaa gaaactggga 540
 atgattgccg gcgggacagg aatcacccca atgctacagc tgatccgggc catcctgaaa 600
 gtccctgaag atccaaccca gtgctttctg ctttttgcca accagacaga aaaggatatc 660
 atcttgccgg aggacttaga ggaactgcag gcccgctatc ccaatcgctt taagctctgg 720
 ttcactctgg atcatcccc aaaagattgg gcctacagca agggctttgt gactgccgac 780
 atgatccggg aacacctgcc cgctccaggg gatgatgtgc tggactgct ttgtgggcca 840
 ccccaatgg tgcagctggc ctgccatccc aacttggaca aactgggcta ctacaaaaag 900
 atgcgattca cctac 915

<210> 104

<211> 681

<212> DNA

<213> Homo sapiens

<400> 104

atgggttga caatgaggct ggtcacagca gcactgttac tgggtctcat gatggtggtc 60
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 ctctttigcc agggccttga agttttctac ccagagttgg ggaacatigg ctgcaaggtt 180
 gttcctgatt gtaacaacta cagacagaag atcacctcct ggalggagcc gatagtcaag 240
 tccccggggg ccgtggacgg cgcaacctat atccttgtga tggatgatcc agatccccct 300
 agcagagcag aaccagaca gagattctgg agacattggc tggtaacaga tatcaagggc 360
 gccgacctga agaaaggga gattcagggc caggagttat cagcciacca ggctccctcc 420
 ccaccggcac acagtggctt ccacgctac cagttctttg tctatcttca ggaaggaaaa 480
 gtcactcttc tcttcccaa ggaaaacaaa actcgaggct cttggaaaat ggacagattt 540

216/307

ctgaaccgtt tccacctggg cgaacctgaa gcaagcacc agttcatgac ccagaactac 600
 caggactcac caacctcca ggctcccaga gaaaggcca gcgagcccaa gcacaaaaac 660
 caggcggaga tagctgcctg c 681

<210> 105

<211> 1323

<212> DNA

<213> Homo sapiens

<400> 105

atggccatcc acaaagcctt ggtgatgtgc ctgggactgc ctctcttctt gttcccaggg 60
 gcctggggccc agggccatgt cccaccgggc tgcagccaag gcctcaacc cctgtactac 120
 aacctgtgtg accgctctgg ggcggtggggc atcgctctgg aggcctgtgc tggggcgggc 180
 atlgtcacca cgtttgtgt caccatcatc ctgggtggcca gcctcccctt tgtgcaggac 240
 accaagaaac ggagcctgct ggggaccag gtattcttcc ttctggggac cctgggcctc 300
 ttctgcctcg tglttgccig tgtggigaag cccgacttct ccacctgtgc ctctcggcgc 360
 ttctctttg gggttctgtt cgccatctgc ttctcttgc tggcggtca cgtctttgcc 420
 ctcaacttcc tggcccgga gaaccacggg ccccggggt gggatgatt cactgtggct 480
 ctgctgtga ccttggtaga ggtcatcatc aatacagagt ggctgatcat caccctggtt 540
 cggggcagtg gcgagggcgg cctcagggc aacagcagcg caggctgggc cgtggcctcc 600
 cctgtgcca tcgccaacat ggactttgtc atggcactca tctacgtcat gctgctgtg 660
 ctgggtgctt tctgggggc ctggccgcc ctgtgtggcc gctacaagcg ctggcgtaag 720
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 gtcatgtata cttacggcaa caagcagcac aacagtccta cctgggatga ccccagctg 840
 gccatgccc tcgcccga tgcctgggcc ttctgtctct tctacgtcat ccccaggtc 900
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217/307

ggcggtgggct atgagaccat cctgaaagag cagaagggtc agagcatgtt cgtggagaac 1020
 aaggcctttt ccatggatga gccggttgca gctaagaggc cgggtgtcacc atacagcggg 1080
 tacaatgggc agctgtgac cagtgtgtac cagcccactg agatggccct gatgcacaaa 1140
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 atgggcagtg ccaactcgac cctgcgggct gaagacatgt actcggccca gagccaccag 1260
 gcggccacac cgccgaaaga cggcaagaac tctcaggtct ttagaaaccc ctacgtgtgg 1320
 gac 1323

<210> 106

<211> 795

<212> DNA

<213> Homo sapiens

<400> 106

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 tcggccatcc aagcccttgt ggggttgccg cggccgctgg tcttggcgt cctgcttgtg 120
 tccgcccgtc tatccagtgt tgtatcacgg actgattcac cgagcccaac cgtactcaac 180
 tcacatatit ctaccccaaa tgtgaatgct ttaacacatg aaaaccaaac caaaccttct 240
 atttcccaaa tcagcaccac cctccctccc acgacgagta ccaagaaaag tggaggagca 300
 tctgtgggcc ctcacccctc gcctactcct ctgtctcaag aggaagctga taacaatgaa 360
 gatcctagta tagaggagga ggatcttctc atgtctgaaca gttctccatc cacagccaaa 420
 gacactctag acaatggcga ttatggagaa ccagactatg actggaccac gggccccagg 480
 gacgacgacg agtctgatga caccttgga gaaaacaggg gttacatgga aattgaacag 540
 tcagtgaat cttttaagat gccatcctca aatatagaag aggaagacag ccatttcttt 600
 ttctatctta ttatttttgc tttttgcatt gctgttgttt acattacata tcacaacaaa 660
 aggaagattt ttcttctggg tcaaagcagg aaatggcglt atggccittg ttccaaaaca 720

218/307

gtggaatacc atgcctaga tcagaatgtt aatgaggcaa tgccttcttt gaagattacc 780

aatgattata ttttt 795

<210> 107

<211> 624

<212> DNA

<213> Homo sapiens

<400> 107

atgciggggc tgciggtggc gttgctggcc ctggggctcg ctgtctttgc gctgctggac 60

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gtccgtgacc tgcagctga gcagccttc ccggccgcgc tgcgccctc ggacttgac 180

ctgctgttgc acatgaacaa cgcgcgtac ctgcgcgagg ccgacttgc gcgcgtcg 240

cacctgacc gctgcggggt gctcggggcg ctgaggaggt tgcgggcga cacgglctg 300

gcggcctcgt gcgcgcgcca ccgcgcctcg ctgcgcctgc tggagccctt cgaggtgcgc 360

acccgcctgc tgggctggga cgaccgcgcg ttctacctgg aggcgcgctt tgcagcctg 420

cgggacggtt tegtgtgcgc gctgctgcgc ttccggcagc acctgtggg cacctcacc 480

gagcgcgtcg tgcagcacct gtgccagcgc aggggtggagc cccctgagct gcccgctgat 540

ctgcagcact ggatctccta caacgaggcc agcagccagc tgcctcccat ggagagtggg 600

ctcagtgatg tcaccaagga ccag 624

<210> 108

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 108

219/307

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 ctgcacctgg ccctgtgcgt gcccggggcc cggggccggg ctctcgagt gttctcgccc 120
 gtggtaaaca tcgagtacgt ggaccgcag accaacctga cgggtgtggag cgtctcgag 180
 agtggccgct tcggcgacag ctgcaccaag gagggcgcg atggcclggg gggcgtccc 240
 tgggcgccc gggagacct cgagggtgc gcgccgaca cgcgttctt cgtgcccag 300
 cccggcgccc gagggcgcg gccctgggtc gccctgggtg ctctggggg ctgcacctt 360
 aaggacaagg tgctgttggc ggcgcggagg aacgcctcgg ccgtcgtcct ctacaatgag 420
 gagcgtacg ggaacatcac cttgccatg tctcacgagg gaacaggaaa tatagtggc 480
 attatgatta gclatccaaa aggaagagaa attttggagc tggtgcaaaa aggaattcca 540
 gtaacgalga ccataggggt tggcaccgg catgtacagg agtcatcag cggtcagtct 600
 gtgggtgttg tggccattgc ctctcacc atgatgatta tctcgttagc ctggctaata 660
 ttttactata tacagcgtt cctatatact ggctctcaga ttggaagtca gagccataga 720
 aaagaaacta agaaagttat tggccagctt ctacttcata ctglaaagca tggagaaaag 780
 ggaattgatg ttgatgctga aaattgtgca gtgtgtatg aaaatttcaa agtaaaggat 840
 attattagaa ttctgccatg caagcatatt ttcatagaa tatgcattga cccatggctt 900
 ttggatcacc gaacatgtcc aatgtglaaa ctgatgtca tcaaagccct aggatattgg 960
 ggagagcctg gggatgtaca ggagatgcct gctccagaat ctctcctgg aagggatcca 1020
 gctgcaaatt tgagtctagc ttaccagat gatgacggaa gtgagagag cagtccacca 1080
 tcagcctccc ctgcgaatc tgagccacag tgtgatccca gctttaaagg agatgcagga 1140
 gaaaatacgg cattgctaga agccggcagg agtgactctc ggcattggagg acccatctcc 1200

<210> 109

<211> 576

<212> DNA

<213> Homo sapiens

220/307

<400> 109

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 aatgacttga atgtttcccc gcctgagcta acagtcctatg tgggtgattc agctctgatg 120
 ggatgtgttt tccagagcac agaagacaaa tgtatattca agatagactg gactctgtca 180
 ccaggagagc acgccaagga cgaatatgtg ctatactatt actccaatct cagtgtgcct 240
 attgggcgct tccagaaccg cgtacacttg atgggggaca acttatgcaa tgatggctct 300
 ctctgtctcc aagatgtgca agaggctgac cagggaacct atatctgtga aatccgcctc 360
 aaaggggaga gccagggtgt caagaaggcg gtggtactgc atgtgcttcc agaggagccc 420
 aaagagctca tgggtccatgt ggggtgattg attcagatgg gatgtgtttt ccagagcaca 480
 gaagtgaaac acgtgaccaa ggtagaatgg atattttcag gacggcgcgc aaaggtaaca 540
 aggaggaaac atcactgtgt tagagaaggc tctggc 576

<210> 110

<211> 780

<212> DNA

<213> Homo sapiens

<400> 110

atggcggggt cgcgcctgct ctggggggcg cgggcggggg gcgtcggcct tttggtgctg 60
 ctgtctgctg gcctgtttcg gcgcgcgcgc gcgctctgcg cgcggccggt aaaggagccc 120
 cgcggcctaa gcgcagcgtc tccgcccttg gctgagactg gcgctcctcg ccgcttcggg 180
 cggtcagtgc cccgaggtga ggcgggcggg gcggtgcagg agctggcgcg gcgcctggcg 240
 catctgctgg aggccgaacg tcaggagcgg gcgcggggcg aggcgagga ggctgaggat 300
 cagcaggcgc gcgtcctggc gcagctgctg cgcgtctggg gcgcgcgcgc caactctgat 360
 ccggctcttg gcctggacga cgaccccgac gcgcctgcag cgcagctcgc tcgcgctctg 420
 ctccgcgcgc gcctlgaccc lgccgccttc gcagcccagc ttgtccccgc gcccgctccc 480

221/307

gccgcggcgc tccgaccccg gcccccggtc tacgacgacg gccccgcggg cccggatgct 540
gaggaggcag gcgacgagac acccgacgtg gaccccgagc tgttgaggta cttgctggga 600
cggattcttg cgggaagcgc ggactccgag ggggtggcag ccccgcgccg cctccgccgt 660
gccgccgacc acgatgtggg ctctgagctg cccctgagg gcgtgctggg ggcgtgctg 720
cgtgtgaaac gcctagagac cccggcgccc caggtgcctg cagccgcct cttgccaccc 780

<210> 111

<211> 1633

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (68)... (1498)

<400> 111

acaaccggct ggggtccttg cgcgcccgcg ctcagggagg agcaccgact gcgccgcacc 60

ctgagag atg gtt ggt gcc atg tgg aag gtg att gtt tcg ctg gtc ctg 109

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu

1 5 10

ttg atg cct ggc ccc tgt gat ggg ctg ttt cgc tcc cta tac aga agt 157

Leu Met Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser

15 20 25 30

gtt tcc atg cca cct aag gga gac tca gga cag cca tta ttt ctc acc 205

Val Ser Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr

35 40 45

cct tac att gaa gct ggg aag atc caa aaa gga aga gaa ttg agt ttg 253

222/307

Pro Tyr Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu
 50 55 60
 gtc ggc cct ttc cca gga ctg aac atg aag agt tat gcc ggc ttc ctc 301
 Val Gly Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu
 65 70 75
 acc gtg aat aag act tac aac agc aac ctc ttc ttc tgg ttc ttc cca 349
 Thr Val Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro
 80 85 90
 gct cag ata cag cca gaa gat gcc cca gla gtt ctc tgg cta cag ggt 397
 Ala Gln Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly
 95 100 105 110
 ggg ccg gga ggt tca tcc atg ttt gga ctc ttt gtg gaa cat ggg cct 445
 Gly Pro Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro
 115 120 125
 tat gtt gtc aca agt aac atg acc ttg cgt gac aga gac ttc ccc tgg 493
 Tyr Val Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp
 130 135 140
 acc aca acg ctc tcc atg ctt tac att gac aat cca gtg ggc aca ggc 541
 Thr Thr Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly
 145 150 155
 ttc agt ttt act gat gat acc cac gga tat gca gtc aat gag gac gat 589
 Phe Ser Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp
 160 165 170
 gta gca cgg gat tta tac agt gca cta att cag ttt ttc cag ata ttt 637
 Val Ala Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe

223/307

175 180 185 190
cct gaa tat aaa aat aat gac ttt tat gtc act ggg gag tct tat gca 685
Pro Glu Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala
 195 200 205
ggg aaa tat gtg cca gcc att gca cac ctc atc cat tcc ctc aac cct 733
Gly Lys Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro
 210 215 220
gtg aga gag gtg aag atc aac ctg aac gga att gct att gga gat gga 781
Val Arg Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly
 225 230 235
tat tct gat ccc gaa tca att ata ggg ggc tat gca gaa ttc ctg tac 829
Tyr Ser Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr
 240 245 250
caa att ggc ttg ttg gat gag aag caa aaa aag tac ttc cag aag cag 877
Gln Ile Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln
255 260 265 270
tgc cat gaa tgc ata gaa cac atc agg aag cag aac tgg ttt gag gcc 925
Cys His Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala
 275 280 285
ttt gaa ata ctg gat aaa cta cta gat ggc gac tta aca agt gat cct 973
Phe Glu Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro
 290 295 300
tct tac ttc cag aat gtt aca gga tgt agt aat tac tat aac ttt ttg 1021
Ser Tyr Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu
 305 310 315

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cgg tgc acg gaa cct gag gat cag ctt tac tat gtg aaa ttt ttg tca 1069
Arg Cys Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser
320 325 330
ctc cca gag gtg aga caa gcc atc cac gtg ggg aat cag act ttt aat 1117
Leu Pro Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn
335 340 345 350
gat gga act ata gtt gaa aag tac ttg cga gaa gat aca gta cag tca 1165
Asp Gly Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser
355 360 365
gtt aag cca tgg tta act gaa atc atg aat aat tat aag gtt ctg atc 1213
Val Lys Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile
370 375 380
tac aat ggc caa ctg gac atc atc gtg gca gct gcc ctg aca gag cac 1261
Tyr Asn Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu His
385 390 395
tcc ttg atg ggc atg gac tgg aaa gga tcc cag gaa tac aag aag gca 1309
Ser Leu Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala
400 405 410
gaa aaa aaa gtt tgg aag atc ttt aaa tct gac agt gaa gtg gct ggt 1357
Glu Lys Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly
415 420 425 430
tac atc cgg caa gcg ggt gac ttc cat cag gta att att cga ggt gga 1405
Tyr Ile Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly
435 440 445
gga cat att tta ccc tat gac cag cct ctg aga gct ttt gac atg att 1453

225/307

Gly His Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile

450

455

460

aat cga ttc att tat gga aaa gga tgg gat cct tat gtt gga taaac 1500

Asn Arg Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly

465

470

475

taccitccca aaagagaaca tcagaggttt tcattgctga aaagaaaatc gtaaaaacag 1560

aaaatgtcat aggaataaaa aaattatctt ttcatatctg caagatTTTT ttcatcaata 1620

aaaattatcc ttg 1633

<210> 112

<211> 1095

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (192)... (872)

<400> 112

ctttaaagt tcatggtaa accatacttg atcctaaatt cctgtacttc ctcaggccat 60

ccgagcatga aacgtgtica cctaccaca tccgtggct gtgacgttg tcaaagtgtt 120

ctctatcggc tgcattgcta gaccacaaa gcgttctgac cggacagtgt cactggagaa 180

ggcggcgca c atg tcc agg gcg cag atc tgg gct ctg gtg tct ggt gtc 230

Met Ser Arg Ala Gln Ile Trp Ala Leu Val Ser Gly Val

1

5

10

gga ggg ttt gga gct ctc gtt gct gct acc acg tcc aat gag tgg aaa 278

Gly Gly Phe Gly Ala Leu Val Ala Ala Thr Thr Ser Asn Glu Trp Lys

226/307

15 20 25
gtg acc acg cga gcc tcc tcg gtg ata aca gcc act tgg gtt tac cag 326
Val Thr Thr Arg Ala Ser Ser Val Ile Thr Ala Thr Trp Val Tyr Gln
30 35 40 45
ggg ctg tgg atg aac tgc gca ggt aac gcg ttg ggt tct ttc cat tgc 374
Gly Leu Trp Met Asn Cys Ala Gly Asn Ala Leu Gly Ser Phe His Cys
50 55 60
cga ccg cat ttt act atc ttc aaa gta gca ggt tat ata cag gca tgt 422
Arg Pro His Phe Thr Ile Phe Lys Val Ala Gly Tyr Ile Gln Ala Cys
65 70 75
aga gga ctt atg atc gct gct gtc agc ctg ggc ttc ttt ggt tcc ata 470
Arg Gly Leu Met Ile Ala Ala Val Ser Leu Gly Phe Phe Gly Ser Ile
80 85 90
ttt gcg ctc ttt gga atg aag tgt acc aaa gtc gga ggc tcc gat aaa 518
Phe Ala Leu Phe Gly Met Lys Cys Thr Lys Val Gly Gly Ser Asp Lys
95 100 105
gcc aaa gct aaa att gct tgt ttg gct ggg att gta ttc ata ctg tca 566
Ala Lys Ala Lys Ile Ala Cys Leu Ala Gly Ile Val Phe Ile Leu Ser
110 115 120 125
ggg ctg tgc tca atg act gga tgt tcc cta tat gca aac aaa atc aca 614
Gly Leu Cys Ser Met Thr Gly Cys Ser Leu Tyr Ala Asn Lys Ile Thr
130 135 140
acg gaa ttc ttt gat cct ctc ttt gtt gag caa aag tat gaa tta gga 662
Thr Glu Phe Phe Asp Pro Leu Phe Val Glu Gln Lys Tyr Glu Leu Gly
145 150 155

227/307

gcc gct ctg ttt att gga tgg gca gga gcc tca ctg tgc ata att ggt 710

Ala Ala Leu Phe Ile Gly Trp Ala Gly Ala Ser Leu Cys Ile Ile Gly

160

165

170

ggg gtc ata ttt tgc ttt tca ata tct gac aac aac aaa aca ccc aga 758

Gly Val Ile Phe Cys Phe Ser Ile Ser Asp Asn Asn Lys Thr Pro Arg

175

180

185

tac aca tac aac ggg gcc aca tct gtc atg tct tct cgg aca aag tat 806

Tyr Thr Tyr Asn Gly Ala Thr Ser Val Met Ser Ser Arg Thr Lys Tyr

190

195

200

205

cat ggt gga gaa gat ttt aaa aca aca aac cct tca aaa cag ttt gat 854

His Gly Gly Glu Asp Phe Lys Thr Thr Asn Pro Ser Lys Gln Phe Asp

210

215

220

aaa aat gct tat gtc t aaaagagctc gcgggcaagc tgcctcttga 900

Lys Asn Ala Tyr Val

225

gtttgttata aaagcgaact gttcacaaaa tgateccatc aaggccctcc cataattaac 960

actcaaaact atttttaaaa tatgcatttg aagcatcigt tgattgtatg gatgtaagtg 1020

tctttacata gttagttata tactaatcat tttctgttgt ggctttctat aaaaaataaa 1080

cagtttatit acagg 1095

<210> 113

<211> 1602

<212> DNA

<213> Homo sapiens

<220>

228/307

<221> CDS

<222> (34)...(951)

<400> 113

ttgtcaggt ggtggaggaa aaggcgctcc gtc atg ggg atc cag acg agc ccc 54

Met Gly Ile Gln Thr Ser Pro

1

5

gtc ctg ctg gcc tcc ctg ggg gtg ggg ctg gtc act ctg ctc ggc ctg 102

Val Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr Leu Leu Gly Leu

10

15

20

gct gtg ggc tcc tac ttg gtt cgg agg tcc cgc cgg cct cag gtc act 150

Ala Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg Pro Gln Val Thr

25

30

35

ctc ctg gac ccc aat gaa aag tac ctg cta cga ctg cta gac aag acg 198

Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr

40

45

50

55

act gtg agc cac aac acc aag agg ttc cgc ttt gcc ctg ccc acc gcc 246

Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala Leu Pro Thr Ala

60

65

70

cac cac act ctg ggg ctg cct gtg ggc aaa cat atc tac ctc tcc acc 294

His His Thr Leu Gly Leu Pro Val Gly Lys His Ile Tyr Leu Ser Thr

75

80

85

cga att gat ggc agc ctg gtc atc agg cca tac act cct gtc acc agt 342

Arg Ile Asp Gly Ser Leu Val Ile Arg Pro Tyr Thr Pro Val Thr Ser

90

95

100

gat gag gat caa ggc tat gtg gat ctt gtc atc aag gtc tac ctg aag 390

229/307

Asp Glu Asp Gln Gly Tyr Val Asp Leu Val Ile Lys Val Tyr Leu Lys
 105 110 115
 ggt gtg cac ccc aaa ttt cct gag gga ggg aag atg tct cag tac ctg 438
 Gly Val His Pro Lys Phe Pro Glu Gly Gly Lys Met Ser Gln Tyr Leu
 120 125 130 135
 gat agc ctg aag gtt ggg gat gtg gtg gag ttt cgg ggg cca agc ggg 486
 Asp Ser Leu Lys Val Gly Asp Val Val Glu Phe Arg Gly Pro Ser Gly
 140 145 150
 ttg ctc act tac act gga aaa ggg cat ttt aac att cag ccc aac aag 534
 Leu Leu Thr Tyr Thr Gly Lys Gly His Phe Asn Ile Gln Pro Asn Lys
 155 160 165
 aaa tct cca cca gaa ccc cga gtg gcg aag aaa ctg gga atg att gcc 582
 Lys Ser Pro Pro Glu Pro Arg Val Ala Lys Lys Leu Gly Met Ile Ala
 170 175 180
 ggc ggg aca gga atc acc cca atg cta cag ctg atc cgg gcc atc ctg 630
 Gly Gly Thr Gly Ile Thr Pro Met Leu Gln Leu Ile Arg Ala Ile Leu
 185 190 195
 aaa gtc cct gaa gat cca acc cag tgc ttt ctg ctt ttt gcc aac cag 678
 Lys Val Pro Glu Asp Pro Thr Gln Cys Phe Leu Leu Phe Ala Asn Gln
 200 205 210 215
 aca gaa aag gat atc atc ttg cgg gag gac tta gag gaa ctg cag gcc 726
 Thr Glu Lys Asp Ile Ile Leu Arg Glu Asp Leu Glu Glu Leu Gln Ala
 220 225 230
 cgc tat ccc aat cgc ttt aag ctc tgg ttc act ctg gat cat ccc cca 774
 Arg Tyr Pro Asn Arg Phe Lys Leu Trp Phe Thr Leu Asp His Pro Pro

230/307

235	240	245	
aaa gat tgg gcc tac agc aag ggc ttt gtg act gcc gac atg atc cgg			822
Lys Asp Trp Ala Tyr Ser Lys Gly Phe Val Thr Ala Asp Met Ile Arg			
250	255	260	
gaa cac ctg ccc gct cca ggg gat gat gtg ctg gta ctg ctt tgt ggg			870
Glu His Leu Pro Ala Pro Gly Asp Asp Val Leu Val Leu Leu Cys Gly			
265	270	275	
cca ccc cca atg gtg cag ctg gcc tgc cat ccc aac ttg gac aaa ctg			918
Pro Pro Pro Met Val Gln Leu Ala Cys His Pro Asn Leu Asp Lys Leu			
280	285	290	295
ggc tac tca caa aag atg cga ttc acc tac tg agcatcctcc agcttcctg			970
Gly Tyr Ser Gln Lys Met Arg Phe Thr Tyr			
300	305		
gtgctgttcg ctgcagttgt tccccatcag tactcaagca ctataagcct tagattcctt			1030
tcctcagagt ttcaggtttt ttcagttaca tctagagctg aaatctggat agtacctgca			1090
ggaacaatat tctgtagcc atggaagagg gccaaaggctc agtcactcct tggatggcct			1150
cctaaatctc cccgtggcaa caggltccagg agaggcccat ggagcagtct cttccatgga			1210
gtaagaagga agggagcatg tacgcttggt ccaagattgg ctagttcctt gatagcatct			1270
tactctcacc ttctttgtgt ctgtgatgaa aggaacagtc tgtgcaatgg gttttactta			1330
aacttcactg ttcaacctat gagcaaatct gtatgtgtga gtataagttg agcatagcat			1390
acttccagag gtggtcttat ggagatggca agaaaggagg aaatgatttc ttcagatctc			1450
aaaggagtct gaaatatcat atttctgtgt gtgtctctct cagccctgc ccaggctaga			1510
gggaaacagc tactgataat cgaaaactgc tgtttgtggc aggaaccctt ggctgtgcaa			1570
ataaatgggg ctgaggcccc tgtlglatat tg			1602

231/307

<210> 114

<211> 897

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (99)... (782)

<400> 114

agtcctccca aagtacttgt gtccgggtgg tggactggat tcgctgcgga gccctggaag 60

ctgcctttcc ttctccctgt gcttaaccag aggtgccc atg ggt tgg aca atg 113

Met Gly Trp Thr Met

1 5

agg ctg glc aca gca gca ctg tta ctg ggt ctc atg atg gtg gtc act 161

Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu Met Met Val Val Thr

10 15 20

gga gac gag gat gag aac agc ccg tgt gcc cat gag gcc ctc ttg gac 209

Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His Glu Ala Leu Leu Asp

25 30 35

gag gac acc ctc ttt tgc cag ggc ctt gaa gtt ttc tac cca gag ttg 257

Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val Phe Tyr Pro Glu Leu

40 45 50

ggg aac att ggc tgc aag gtt gtt cct gat tgt aac aac tac aga cag 305

Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys Asn Asn Tyr Arg Gln

55 60 65

aag atc acc tcc tgg atg gag ccg ata gtc aag ttc ccg ggg gcc glg 353

232/307

Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys Phe Pro Gly Ala Val
70 75 80 85
gac ggc gca acc tat atc ctg gtg atg gtg gat cca gat gcc cct agc 401
Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp Pro Asp Ala Pro Ser
90 95 100
aga gca gaa ccc aga cag aga ttc tgg aga cat tgg ctg gta aca gat 449
Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His Trp Leu Val Thr Asp
105 110 115
atc aag ggc gcc gac ctg aag aaa ggg aag att cag ggc cag gag tta 497
Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile Gln Gly Gln Glu Leu
120 125 130
tea gcc tac cag gct ccc tcc cca ccg gca cac agt ggc ttc cat cgc 545
Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His Ser Gly Phe His Arg
135 140 145
tac cag ttc ttt gtc tat ctt cag gaa gga aaa gtc atc tct ctc ctt 593
Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys Val Ile Ser Leu Leu
150 155 160 165
ccc aag gaa aac aaa act cga ggc tct tgg aaa atg gac aga ttt ctg 641
Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys Met Asp Arg Phe Leu
170 175 180
aac cgt ttc cac ctg ggc gaa cct gaa gca agc acc cag ttc atg acc 689
Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser Thr Gln Phe Met Thr
185 190 195
cag aac tac cag gac tca cca acc ctc cag gct ccc aga gaa agg gcc 737
Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala Pro Arg Glu Arg Ala

233/307

200 205 210
 agc gag ccc aag cac aaa aac cag gcg gag ata gct gcc tgc t 780
 Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile Ala Ala Cys

215 220 225
 agatagccgg ctttgccatc cgggcatgtg gccacactgc ccaccaccga cgatgtgggt 840
 atggaacccc ctctggatac agaaccctt cttttccaaa taaaaaaaaa atcatcc 897

<210> 115

<211> 1866

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (142)... (1467)

<400> 115

gcccgcattgc gggggcggtgg cagtcaacag caacaaccca cagccggca gggccagaaa 60
 ctcccatctc cctcaccagc cggaagtag gagtcggctc agcctggagg gacccaacca 120
 gagcctggcc tgggagccag g atg gcc atc cac aaa gcc ttg gtg atg tgc 171

Met Ala Ile His Lys Ala Leu Val Met Cys

1 5 10
 ctg gga ctg cct ctc ttc ctg ttc cca ggg gcc tgg gcc cag ggc cat 219
 Leu Gly Leu Pro Leu Phe Leu Phe Pro Gly Ala Trp Ala Gln Gly His

15 20 25
 gtc cca ccc ggc tgc agc caa ggc ctc aac ccc ctg tac tac aac ctg 267
 Val Pro Pro Gly Cys Ser Gln Gly Leu Asn Pro Leu Tyr Tyr Asn Leu

234/307

30	35	40	
tgt gac cgc tct ggg gcg tgg ggc atc gtc ctg gag gcc gtg gct ggg	315		
Cys Asp Arg Ser Gly Ala Trp Gly Ile Val Leu Glu Ala Val Ala Gly			
45	50	55	
gcg ggc att gtc acc acg ttt gtg ctc acc atc atc ctg gtg gcc agc	363		
Ala Gly Ile Val Thr Thr Phe Val Leu Thr Ile Ile Leu Val Ala Ser			
60	65	70	
ctc ccc ttt gtg cag gac acc aag aaa cgg agc ctg ctg ggg acc cag	411		
Leu Pro Phe Val Gln Asp Thr Lys Lys Arg Ser Leu Leu Gly Thr Gln			
75	80	85	90
gta ttc ttc ctt ctg ggg acc ctg ggc ctc ttc tgc ctc gtg ttt gcc	459		
Val Phe Phe Leu Leu Gly Thr Leu Gly Leu Phe Cys Leu Val Phe Ala			
95	100	105	
tgt gtg gtg aag ccc gac ttc tcc acc tgt gcc tct cgg cgc ttc ctc	507		
Cys Val Val Lys Pro Asp Phe Ser Thr Cys Ala Ser Arg Arg Phe Leu			
110	115	120	
ttt ggg gtt ctg ttc gcc atc tgc ttc tct tgt ctg gcg gct cac gtc	555		
Phe Gly Val Leu Phe Ala Ile Cys Phe Ser Cys Leu Ala Ala His Val			
125	130	135	
ttt gcc ctc aac ttc ctg gcc cgg aag aac cac ggg ccc cgg ggc tgg	603		
Phe Ala Leu Asn Phe Leu Ala Arg Lys Asn His Gly Pro Arg Gly Trp			
140	145	150	
gtg atc ttc act gtg gct ctg ctg ctg acc ctg gta gag gtc atc atc	651		
Val Ile Phe Thr Val Ala Leu Leu Leu Thr Leu Val Glu Val Ile Ile			
155	160	165	170

235/307

aat aca gag tgg ctg atc atc acc ctg gtt cgg ggc agt ggc gag ggc 699
 Asn Thr Glu Trp Leu Ile Ile Thr Leu Val Arg Gly Ser Gly Glu Gly
 175 180 185
 ggc cct cag ggc aac agc agc gca ggc tgg gcc gtg gcc tcc ccc tgt 747
 Gly Pro Gln Gly Asn Ser Ser Ala Gly Trp Ala Val Ala Ser Pro Cys
 190 195 200
 gcc atc gcc aac atg gac ttt gtc atg gca ctc atc tac gtc atg ctg 795
 Ala Ile Ala Asn Met Asp Phe Val Met Ala Leu Ile Tyr Val Met Leu
 205 210 215
 ctg ctg ctg ggt gcc ttc ctg ggg gcc tgg ccc gcc ctg tgt ggc cgc 843
 Leu Leu Leu Gly Ala Phe Leu Gly Ala Trp Pro Ala Leu Cys Gly Arg
 220 225 230
 tac aag cgc tgg cgt aag cat ggg gtc ttt gtg ctc ctc acc aca gcc 891
 Tyr Lys Arg Trp Arg Lys His Gly Val Phe Val Leu Leu Thr Thr Ala
 235 240 245 250
 acc tcc gtt gcc ata tgg gtg gtg tgg atc gtc atg tat act tac ggc 939
 Thr Ser Val Ala Ile Trp Val Val Trp Ile Val Met Tyr Thr Tyr Gly
 255 260 265
 aac aag cag cac aac agt ccc acc tgg gat gac ccc acg ctg gcc atc 987
 Asn Lys Gln His Asn Ser Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile
 270 275 280
 gcc ctc gcc gcc aat gcc tgg gcc ttc gtc ctc ttc tac gtc atc ccc 1035
 Ala Leu Ala Ala Asn Ala Trp Ala Phe Val Leu Phe Tyr Val Ile Pro
 285 290 295
 gag gtc tcc cag gtg acc aag tcc agc cca gag caa agc tac cag ggg 1083

236/307

Glu Val Ser Gln Val Thr Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly
 300 305 310
 gac atg tac ccc acc cgg ggc gtg ggc tat gag acc atc ctg aaa gag 1131
 Asp Met Tyr Pro Thr Arg Gly Val Gly Tyr Glu Thr Ile Leu Lys Glu
 315 320 325 330
 cag aag ggt cag agc atg ttc gtg gag aac aag gcc ttt tcc atg gat 1179
 Gln Lys Gly Gln Ser Met Phe Val Glu Asn Lys Ala Phe Ser Met Asp
 335 340 345
 gag ccg gtt gca gct aag agg ccg gtg tca cca tac agc ggg tac aat 1227
 Glu Pro Val Ala Ala Lys Arg Pro Val Ser Pro Tyr Ser Gly Tyr Asn
 350 355 360
 ggg cag ctg ctg acc agt gtg tac cag ccc act gag atg gcc ctg atg 1275
 Gly Gln Leu Leu Thr Ser Val Tyr Gln Pro Thr Glu Met Ala Leu Met
 365 370 375
 cac aaa gtt ccg tcc gaa gga gct tac gac atc atc ctc cca cgg gcc 1323
 His Lys Val Pro Ser Glu Gly Ala Tyr Asp Ile Ile Leu Pro Arg Ala
 380 385 390
 acc gcc aac agc cag gtg atg ggc agt gcc aac tcg acc ctg cgg gct 1371
 Thr Ala Asn Ser Gln Val Met Gly Ser Ala Asn Ser Thr Leu Arg Ala
 395 400 405 410
 gaa gac atg tac tcg gcc cag agc cac cag gcg gcc aca ccg ccg aaa 1419
 Glu Asp Met Tyr Ser Ala Gln Ser His Gln Ala Ala Thr Pro Pro Lys
 415 420 425
 gac ggc aag aac tct cag gtc ttt aga aac ccc tac gtg tgg gac 1464
 Asp Gly Lys Asn Ser Gln Val Phe Arg Asn Pro Tyr Val Trp Asp

237/307

430	435	440	
tgagtc agcgggtggcg aggagaggcg gtcggatttg gggagggccc tgaggacctg			1520
gccccggggca agggactctc caggctcctc ctccccctgg caggcccagc aacatgtgcc			1580
ccagatgtgg aagggcctcc ctctctgccca gtgtttgggt ggggtgcatg ggtgtcccca			1640
cccactcctc agtgtttgtg gagtcgagga gccaacccca gcctcctgcc aggatcacct			1700
cggcggtcac actccagcca aatagtgttc tcgggggtgg ggctgggcag cgcctatgtt			1760
tctctggaga ttctgcaac ctcaagagac ttcccaggcg ctccaggcctg gatcttctc			1820
ctctgtgagg aacaagggtg cctaataaat acatttctgc ttatt			1866

<210> 116

<211> 2198

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)... (847)

<400> 116

aaaatggcgt agagcctagc aacagcgcag gctcccagcc gagtcggt atg gcc	55
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Met Ala

1

gct gcc gtc ccg aag agg atg agg ggg cca gca caa gcg aaa ctg ctg	103
---	-----

Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys Leu Leu

5

10

15

ccc ggg tcg gcc atc caa gcc ctt gtg ggg ttg gcg cgg ccg ctg gtc	151
---	-----

Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro Leu Val

238/307

20 25 30
ttg gcg ctc ctg ctt gtg tcc gcc gct cta tcc agt gtt gta tca cgg 199
Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val Ser Arg
35 40 45 50
act gat tca ccg agc cca acc gta ctc aac tca cat att tct acc cca 247
Thr Asp Ser Pro Ser Pro Thr Val Leu Asn Ser His Ile Ser Thr Pro
55 60 65
aat gtg aat gct tta aca cat gaa aac caa acc aaa cct tct att tcc 295
Asn Val Asn Ala Leu Thr His Glu Asn Gln Thr Lys Pro Ser Ile Ser
70 75 80
caa atc agc acc acc ctc cct ccc acg acg agt acc aag aaa agt gga 343
Gln Ile Ser Thr Thr Leu Pro Pro Thr Thr Ser Thr Lys Lys Ser Gly
85 90 95
gga gca tct gtg gtc cct cat ccc tcg cct act cct ctg tct caa gag 391
Gly Ala Ser Val Val Pro His Pro Ser Pro Thr Pro Leu Ser Gln Glu
100 105 110
gaa gct gat aac aat gaa gat cct agt ata gag gag gag gat ctt ctc 439
Glu Ala Asp Asn Asn Glu Asp Pro Ser Ile Glu Glu Glu Asp Leu Leu
115 120 125 130
atg ctg aac agt tct cca tcc aca gcc aaa gac act cta gac aat ggc 487
Met Leu Asn Ser Ser Pro Ser Thr Ala Lys Asp Thr Leu Asp Asn Gly
135 140 145
gat tat gga gaa cca gac tat gac tgg acc acg ggc ccc agg gac gac 535
Asp Tyr Gly Glu Pro Asp Tyr Asp Trp Thr Thr Gly Pro Arg Asp Asp
150 155 160

239/307

gac gag tct gat gac acc ttg gaa gaa aac agg ggt tac atg gaa att 583

Asp Glu Ser Asp Asp Thr Leu Glu Glu Asn Arg Gly Tyr Met Glu Ile

165

170

175

gaa cag tca gtg aaa tct ttt aag atg cca tcc tca aat ata gaa gag 631

Glu Gln Ser Val Lys Ser Phe Lys Met Pro Ser Ser Asn Ile Glu Glu

180

185

190

gaa gac agc cat ttc ttt ttt cat ctt att att ttt gct ttt tgc att 679

Glu Asp Ser His Phe Phe Phe His Leu Ile Ile Phe Ala Phe Cys Ile

195

200

205

210

gct gtt gtt tac att aca tat cac aac aaa agg aag att ttt ctt ctg 727

Ala Val Val Tyr Ile Thr Tyr His Asn Lys Arg Lys Ile Phe Leu Leu

215

220

225

gtt caa agc agg aaa tgg cgt gat ggc ctt tgt tcc aaa aca gtg gaa 775

Val Gln Ser Arg Lys Trp Arg Asp Gly Leu Cys Ser Lys Thr Val Glu

230

235

240

tac cat cgc cta gat cag aat gtt aat gag gca atg cct tct ttg aag 823

Tyr His Arg Leu Asp Gln Asn Val Asn Glu Ala Met Pro Ser Leu Lys

245

250

255

att acc aat gat tat att ttt taaagc actgtgattt gaatttgctt 870

Ile Thr Asn Asp Tyr Ile Phe

260

265

atgiaatttt atttgcttga cttttlatat gatattgtgc aaatgtttgc cataggcaat 930

tggiacttaa atgagagggtg agtctctctt ttgccttggt gctttggaaa ttaaagtca 990

caaacgagta tataattttt tatctgtact tttagagctg agtttaatca ggtgtccaaa 1050

atglgagtta aacattacct tatatttaca ctgttagttt ttattgtttt agatttiatta 1110

240/307

tgctttcttct ggaagtatta gtgatgctac ttttaaaaga tcccaaactt gtaactaaat 1170
tctgacatat ctgttactgc tgactcacat tcattctccg ccattcaaact actatttttt 1230
atccacattt tttttgttc ccaaactgta atgtacaagg atatgtgtga taatgctttg 1290
gatttgagta atattttttt ttcttccaag aaaactgctt tggatatttt tagataattt 1350
aaacataatt taggataatg atattgctca atctgaccac aattttaggt aaaacattaa 1410
atgtgtcaag aaatcttggc aacagagact ctgcagcttg cagtggacat agataaaatg 1470
ttacagagat actatttttt tggttggaat tactatatta aatttagaag cagaaactgg 1530
taaaatgta aatacatgta caattgcttt tagttagcaa ttgattgtag catgggttcc 1590
tccaagggtt caagcaatgg gcagagtta aaattatata agattcgttt acttcgttta 1650
ttattttaca gtaaatttga ataaatctta ggggtcatta tcacttaaat aatactgtac 1710
ctaggtcttt caaatlaaaa ttatactga atgaagttgt ttgtalacat aaaggatatt 1770
tgtgtacaat tacctttttt cccccacact tgtttcttt gttttgttt tttatggcaa 1830
ctggaaagta ttactatgg gattcattta tgtctgctt tctatcataa agaattgatc 1890
aatatgtaaa tatgtgattt gaaccatggt tgacttaca gtgtcactac agcttttttag 1950
aaaacatagc cctaatatat gttaagcagg acccgggtga gccagtgggc ttgcgcttta 2010
tgtagagctg gaagaaggcc gtccatcttg tctcttgggc ggacagtgtg ctttccaat 2070
agggaaggga agcacaatgg aaatacccct gaaccgtttt attgcagtaa ttttttcat 2130
atctgaaact attatttaat attttgaata agattttaaa aaataaatgg caaagatata 2190
aatclatg 2198

<210> 117

<211> 2180

<212> DNA

<213> Homo sapiens

<220>

241/307

<221> CDS

<222> (69)... (695)

<400> 117.

aaccagcgcc gcggacaccg gcaccggcgc cacggactcc gcaggacccc gcgcccgcgc 60

ccgccgct atg ctg ggg ctg ctg gtc gcg ttg ctg gcc ctg ggg ctc gct 110

Met Leu Gly Leu Leu Val Ala Leu Leu Ala Leu Gly Leu Ala

1 5 10

gtc ttt gcg ctg ctg gac gtc tgg tac ctg gtg cgc ctt ccg tgc gcc 158

Val Phe Ala Leu Leu Asp Val Trp Tyr Leu Val Arg Leu Pro Cys Ala

15 20 25 30

gtg ctg cgc gcg cgc ctg ctg cag ccg cgc gtc cgt gac ctg cta gct 206

Val Leu Arg Ala Arg Leu Leu Gln Pro Arg Val Arg Asp Leu Leu Ala

35 40 45

gag cag cgc ttc ccg ggc cgc gtg ctg ccc tcg gac ttg gac ctg ctg 254

Glu Gln Arg Phe Pro Gly Arg Val Leu Pro Ser Asp Leu Asp Leu Leu

50 55 60

ttg cac atg aac aac gcg cgc tac ctg cgc gag gcc gac ttt gcg cgc 302

Leu His Met Asn Asn Ala Arg Tyr Leu Arg Glu Ala Asp Phe Ala Arg

65 70 75

gtc gcg cac ctg acc cgc tgc ggg gtg ctc ggg gcg ctg agg gag ttg 350

Val Ala His Leu Thr Arg Cys Gly Val Leu Gly Ala Leu Arg Glu Leu

80 85 90

cgg gcg cac acg gtg ctg gcg gcc tcg tgc gcg cgc cac cgc cgc tcg 398

Arg Ala His Thr Val Leu Ala Ala Ser Cys Ala Arg His Arg Arg Ser

95 100 105 110

242/307

ctg cgc ctg ctg gag ccc ttc gag gtg cgc acc cgc ctg ctg ggc tgg 446
 Leu Arg Leu Leu Glu Pro Phe Glu Val Arg Thr Arg Leu Leu Gly Trp
 115 120 125
 gac gac cgc gcg ttc tac ctg gag gcg cgc ttt gtc agc ctg cgg gac 494
 Asp Asp Arg Ala Phe Tyr Leu Glu Ala Arg Phe Val Ser Leu Arg Asp
 130 135 140
 ggt ttc gtg tgc gcg ctg ctg cgc ttc cgg cag cac ctg ctg ggc acc 542
 Gly Phe Val Cys Ala Leu Leu Arg Phe Arg Gln His Leu Leu Gly Thr
 145 150 155
 tca ccc gag cgc gtc gtg cag cac ctg tgc cag cgc agg gtg gag ccc 590
 Ser Pro Glu Arg Val Val Gln His Leu Cys Gln Arg Arg Val Glu Pro
 160 165 170
 cct gag ctg ccc gct gat ctg cag cac tgg atc tcc tac aac gag gcc 638
 Pro Glu Leu Pro Ala Asp Leu Gln His Trp Ile Ser Tyr Asn Glu Ala
 175 180 185 190
 agc agc cag ctg ctc cgc atg gag agt ggg ctc agt gat gtc acc aag 686
 Ser Ser Gln Leu Leu Arg Met Glu Ser Gly Leu Ser Asp Val Thr Lys
 195 200 205
 gac cag tgaccgcc accttcacac cgtctgccct ggccaccatc ctgggcctgg 740
 Asp Gln
 gggtgccca cagatgggca gtctcagcca tactctgttc cagctggagt agcctcctga 800
 ccagcctggc ccacctgct ccaccactg ggcccccca gttattgata cccctctgtg 860
 ctgggtccca cgctaggcag aaggaggagt ggcatlggca tcctgaccca gctctgccct 920
 caaggtgggg atggatgggc aaaggagagt cctgcctggc cctacgatga ggccactcat 980
 gtgggcctag gtaggggagg atggcctg gagcagaggg acccacaagt gcctcccag 1040

243/307

cctagatcct ggctcggacc actgcaaggg ccgaggcagg gccagaccag agcatcctgg 1100
gtacaggcct gggctctcca gggcctgggc ctgattcagg tgcagtgggc actcctgaag 1160
ggtcagagcg gcatctgcca ggcagcccct ctggcttccg ctgaggtggg tgcaggcctg 1220
gggcagagcc tgggtgggtca gaggccgggg ctagaggcag atggaaggga ggcatttgct 1280
gacagaggac ggggcacccg ggctcccact gcagtcggcc ttgcctctc ctcctcctct 1340
acctccagtc aggctggacg ggagggtagc cttgtggctg agaggggtca gactaggltg 1400
cacaggggct cctggaaaga cagcaggctt cctgctgggc gtcccttgt tggagggaat 1460
agagtggggg tgggactctg caggggtgtc cttgtccact cgcacccctc gccgccacc 1520
agggccatgc tctgtgactt gggctgatcc ccacccttc tgggcctaca gcaccacagg 1580
ccgctglacc cccttagagc tgccctctc tggcctggcc ggcagacgtc ttcttaactc 1640
ctctgtctc tatattcagc atgttccttg tcagctgctg ggccggccct gccttgctg 1700
agcagagcct ctctggcag cttctcaggt ctccctaatg gagacaccag gclactagga 1760
cactggctgg gccaccccc tctgcctaa tgcctcacct tacagctggg gaaactgagg 1820
cctggaatgg ccagagtca ccaaggcaaa gttggggctg gtccagcct gaggctccag 1880
ctgatgcct cagctcccag agaggggggtg ccccatctag ctgggtgcag gggtcactgc 1940
ttgtcagtc agggccctgt gcccgcttgc ctgtccctt acactgtgc ctgcacatcc 2000
agaactgcct ccttgccgt gccctcagga agcccacctt gagccagagt caagggctgc 2060
agcactgccc gatagaacac gcccgccctc actgctgttc ttgccttaca gccaccatgg 2120
gaaagctgca acctttctgt tttattttaa gaaagcccaa catlaaaggg ttttcattgc 2180

<210> 118

<211> 1527

<212> DNA

<213> Homo sapiens

<220>

244/307

<221> CDS

<222> (103)... (1305)

<400> 118

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cgcgtgaccc tgactccccc tagtcagctc agcgggtgctg cc atg gcg tgg cgg 114

Met Ala Trp Arg

1

cgg cgc gaa gcc agc gtc ggg gct cgc gcc gtg ttg gct ctg gcg ttg 162

Arg Arg Glu Ala Ser Val Gly Ala Arg Gly Val Leu Ala Leu Ala Leu

5 10 15 20

ctc gcc ctg gcc ctg tgc gtg ccc ggg gcc cgg gcc cgg gct ctc gag 210

Leu Ala Leu Ala Leu Cys Val Pro Gly Ala Arg Gly Arg Ala Leu Glu

25 30 35

tgg ttc tcg gcc gtg gta aac atc gag tac gtg gac ccg cag acc aac 258

Trp Phe Ser Ala Val Val Asn Ile Glu Tyr Val Asp Pro Gln Thr Asn

40 45 50

ctg acg gtg tgg agc gtc tcg gag agt gcc cgc ttc gcc gac agc tcg 306

Leu Thr Val Trp Ser Val Ser Glu Ser Gly Arg Phe Gly Asp Ser Ser

55 60 65

ccc aag gag gcc gcg cat gcc ctg gtg gcc gtc ccg tgg gcg ccc gcc 354

Pro Lys Glu Gly Ala His Gly Leu Val Gly Val Pro Trp Ala Pro Gly

70 75 80

gga gac ctc gag gcc tgc gcg ccc gac acg cgc ttc ttc gtg ccc gag 402

Gly Asp Leu Glu Gly Cys Ala Pro Asp Thr Arg Phe Phe Val Pro Glu

85 90 95 100

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ccc ggc ggc cga ggg gcc gcg ccc tgg gtc gcc ctg gtg gct cgt ggg      450
Pro Gly Gly Arg Gly Ala Ala Pro Trp Val Ala Leu Val Ala Arg Gly

      105      110      115
ggc tgc acc ttc aag gac aag gtg ctg gtg gcg gcg cgg agg aac gcc      498
Gly Cys Thr Phe Lys Asp Lys Val Leu Val Ala Ala Arg Arg Asn Ala

      120      125      130
tcg gcc gtc gtc ctc tac aat gag gag cgc tac ggg aac atc acc ttg      546
Ser Ala Val Val Leu Tyr Asn Glu Glu Arg Tyr Gly Asn Ile Thr Leu

      135      140      145
ccc atg tct cac gcg gga aca gga aat ata gtg gtc att atg att agc      594
Pro Met Ser His Ala Gly Thr Gly Asn Ile Val Val Ile Met Ile Ser

      150      155      160
tat cca aaa gga aga gaa att ttg gag ctg gtg caa aaa gga att cca      642
Tyr Pro Lys Gly Arg Glu Ile Leu Glu Leu Val Gln Lys Gly Ile Pro

      165      170      175      180
gta acg atg acc ata ggg gtt ggc acc cgg cat gta cag gag ttc atc      690
Val Thr Met Thr Ile Gly Val Gly Thr Arg His Val Gln Glu Phe Ile

      185      190      195
agc ggt cag tct gtg gtg ttt gtg gcc att gcc ttc atc acc atg atg      738
Ser Gly Gln Ser Val Val Phe Val Ala Ile Ala Phe Ile Thr Met Met

      200      205      210
att atc tcg tta gcc tgg cta ata ttt tac tat ata cag cgt ttc cta      786
Ile Ile Ser Leu Ala Trp Leu Ile Phe Tyr Tyr Ile Gln Arg Phe Leu

      215      220      225
tal act ggc tct cag att gga agt cag agc cat aga aaa gaa act aag      834

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246/307

Tyr Thr Gly Ser Gln Ile Gly Ser Gln Ser His Arg Lys Glu Thr Lys
 230 235 240
 aaa gtt att ggc cag ctt cta ctt cat act gta aag cat gga gaa aag 882
 Lys Val Ile Gly Gln Leu Leu Leu His Thr Val Lys His Gly Glu Lys
 245 250 255 260
 gga att gat gtt gat gct gaa aat tgt gca gtg tgt att gaa aat ttc 930
 Gly Ile Asp Val Asp Ala Glu Asn Cys Ala Val Cys Ile Glu Asn Phe
 265 270 275
 aaa gta aag gat att att aga att ctg cca tgc aag cat att ttt cat 978
 Lys Val Lys Asp Ile Ile Arg Ile Leu Pro Cys Lys His Ile Phe His
 280 285 290
 aga ata tgc att gac cca tgg ctt ttg gat cac cga aca tgt cca atg 1026
 Arg Ile Cys Ile Asp Pro Trp Leu Leu Asp His Arg Thr Cys Pro Met
 295 300 305
 tgt aaa ctt gat gtc atc aaa gcc cta gga tat tgg gga gag cct ggg 1074
 Cys Lys Leu Asp Val Ile Lys Ala Leu Gly Tyr Trp Gly Glu Pro Gly
 310 315 320
 gat gta cag gag atg cct gct cca gaa tct cct cct gga agg gat cca 1122
 Asp Val Gln Glu Met Pro Ala Pro Glu Ser Pro Pro Gly Arg Asp Pro
 325 330 335 340
 gct gca aat ttg agt cta gct tta cca gat gat gac gga agt gat gag 1170
 Ala Ala Asn Leu Ser Leu Ala Leu Pro Asp Asp Asp Gly Ser Asp Glu
 345 350 355
 agc agt cca cca tca gcc tcc cct gct gaa tct gag cca cag tgt gat 1218
 Ser Ser Pro Pro Ser Ala Ser Pro Ala Glu Ser Glu Pro Gln Cys Asp

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360	365	370	
ccc agc ttt aaa gga gat gca gga gaa aat acg gca ttg cta gaa gcc			1266
Pro Ser Phe Lys Gly Asp Ala Gly Glu Asn Thr Ala Leu Leu Glu Ala			
375	380	385	
ggc agg agt gac tct cgg cat gga gga ccc atc tcc tagcacac			1310
Gly Arg Ser Asp Ser Arg His Gly Gly Pro Ile Ser			
390	395	400	
gtgcccactg aaglggcacc aacagaagtt tggcttgaac taaaggacat tttatttttt			1370
ttacttttagc acataatttg tatatttgaa aataatgtat attattttac ctattagatt			1430
ctgatttgat atacaaagga ctaagatatt ttcttcttga agagactttt cgattagtcc			1490
tcatatattt atctactaaa atagagtgtt taccatg			1527

<210> 119

<211> 1905

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (125)... (703)

<400> 119

gagcctaacc tagagtgctc gcagcagctc ttcagttgag cttggggact gcagctgtgg	60
ggagatttca gtgcattgcc tcccctgggt gctcttcac ttggatttga aagttgagag	120
cagc atg ttt tgc cca ctg aaa etc atc ctg ctg cca gtg tta ctg gat	169

Met Phe Cys Pro Leu Lys Leu Ile Leu Leu Pro Val Leu Leu Asp

1 5 10 15

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tat tcc ttg ggc ctg aat gac ttg aat gtt tcc ccg cct gag cta aca	217
Tyr Ser Leu Gly Leu Asn Asp Leu Asn Val Ser Pro Pro Glu Leu Thr	
20 25 30	
gtc cat gtg ggt gat tca gct ctg atg gga tgt gtt ttc cag agc aca	265
Val His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln Ser Thr	
35 40 45	
gaa gac aaa tgt ata ttc aag ata gac tgg act ctg tca cca gga gag	313
Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser Pro Gly Glu	
50 55 60	
cac gcc aag gac gaa tat gtg cta tac tat tac tcc aat ctc agt gtg	361
His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser Asn Leu Ser Val	
65 70 75	
cct att ggg cgc ttc cag aac cgc gta cac ttg atg ggg gac aac tta	409
Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu Met Gly Asp Asn Leu	
80 85 90 95	
tgc aat gat ggc tct ctc ctg ctc caa gat gtg caa gag gct gac cag	457
Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp Val Gln Glu Ala Asp Gln	
100 105 110	
gga acc tat atc tgt gaa atc cgc ctc aaa ggg gag agc cag gtg ttc	505
Gly Thr Tyr Ile Cys Glu Ile Arg Leu Lys Gly Glu Ser Gln Val Phe	
115 120 125	
aag aag gcg gtg gta ctg cat gtg ctt cca gag gag ccc aaa gag ctc	553
Lys Lys Ala Val Val Leu His Val Leu Pro Glu Glu Pro Lys Glu Leu	
130 135 140	
atg gtc cat glg ggt gga ttg att cag atg gga tgt gtt ttc cag agc	601

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Met Val His Val Gly Gly Leu Ile Gln Met Gly Cys Val Phe Gln Ser
 145 150 155
 aca gaa gtg aaa cac gtg acc aag gta gaa tgg ata ttt tca gga cgg 649
 Thr Glu Val Lys His Val Thr Lys Val Glu Trp Ile Phe Ser Gly Arg
 160 165 170 175
 cgc gca aag gta aca agg agg aaa cat cac tgt gtt aga gaa ggc tct 697
 Arg Ala Lys Val Thr Arg Arg Lys His His Cys Val Arg Glu Gly Ser
 180 185 190
 ggc tgatggtatc aggacaaagg tagaatcagg cacatgagga ggtgttgcaa 750
 Gly
 gagcctgggc ttigtgtgctt atcagaactg gaccttctcc tagcaatttc agctttctgg 810
 tgggaaagat aactccaatg aagaacaaga acaagaagat gatgatgatg cttaactttt 870
 tggatgccga tatgagattg tacatgagga gattgtattt cgttaciacc acaaactcag 930
 gatgtctgcg gagtactccc agagctgggg ccacttccag aatcgtgtga acctggtggg 990
 ggacattttc cgcaatgacg gtccatcat gcttcaagga gtgaggaggat cagatggagg 1050
 aaactacacc tgcagtatcc acctagggaa cclggtgttc aagaaaacca ttgtgctgca 1110
 tgtcagcccg gaagagcctc gaacactggt gaccccgga gccctgaggc ctctggtctt 1170
 gggtggtaat cagttggtga tcattglggg aattgtctgt gccacaaacc tgetgtcccc 1230
 tgttctgala ttgatcgtga agaagacctg tggaaataag agttcagtga attctacagt 1290
 cttggtgaag aacacgaaga agactaatcc agagataaaa gaaaaaccct gccattttga 1350
 aagatgtgaa ggggagaaac acatttactc cccaataatt gtacgggagg tgatcgagga 1410
 agaagaacca agtgaaaaat cagaggccac ctacatgacc atgcaccag tttggccttc 1470
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 acagcaagcc ttttgagaag aatggagagt ccttcatct cagcagcggg ggagactctc 1590
 tctgtgtgt gtcttgggcc actctaccag tgatttcaga ctccgcctc cccagctgtc 1650

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ctcctgtctc attgtttggt caatacactg aagatggaga atttggagcc tggcagagag 1710
actggacagc tctggaggaa caggcctgct gaggggaggg gagcatggac ttggcctctg 1770
gagtgggaca ctggccctgg gaaccaggct gagctgagtg gcctcaaacc ccccggttga 1830
tcagaccctc ctgigggcag ggttccttagt ggatgagtta ctgggaagaa tcagagataa 1890
aaaccaaccc aaatc 1905

<210> 120

<211> 998

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)... (832)

<400> 120

gcacttgcca gccagtcgc cgcgccggag cccggctcgc tggggcagc atg ggc 55

Met Ala

ggg tcg ccg ctg ctc tgg ggg ccg cgg gcc ggg ggc gtc ggc ctt ttg 103

Gly Ser Pro Leu Leu Trp Gly Pro Arg Ala Gly Gly Val Gly Leu Leu

5

10

15

gtg ctg ctg ctg ctc ggc ctg ttt cgg ccg ccc ccc ggc ctc tgc ggc 151

Val Leu Leu Leu Leu Gly Leu Phe Arg Pro Pro Pro Ala Leu Cys Ala

20

25

30

cgg ccg gta aag gag ccc cgc ggc cta agc gca ggc tct ccg ccc ttg 199

Arg Pro Val Lys Glu Pro Arg Gly Leu Ser Ala Ala Ser Pro Pro Leu

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35	40	45	50	
gct gag act ggc gct cct cgc cgc ttc cgg cgg tca gtg ccc cga ggt				247
Ala Glu Thr Gly Ala Pro Arg Arg Phe Arg Arg Ser Val Pro Arg Gly				
	55	60	65	
gag gcg gcg ggg gcg gtg cag gag ctg gcg cgg gcg ctg gcg cat ctg				295
Glu Ala Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala His Leu				
	70	75	80	
ctg gag gcc gaa cgt cag gag cgg gcg cgg gcc gag gcg cag gag gct				343
Leu Glu Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln Glu Ala				
	85	90	95	
gag gat cag cag gcg cgc gtc ctg gcg cag ctg ctg cgc gtc tgg ggc				391
Glu Asp Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Val Trp Gly				
	100	105	110	
gcc ccc cgc aac tct gat ccg gct ctg ggc ctg gac gac gac ccc gac				439
Ala Pro Arg Asn Ser Asp Pro Ala Leu Gly Leu Asp Asp Asp Pro Asp				
	115	120	125	130
gcg cct gca gcg cag ctc gct cgc gct ctg ctc cgc gcc cgc ctt gac				487
Ala Pro Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg Leu Asp				
	135	140	145	
cct gcc gcc ctc gca gcc cag ctt gtc ccc gcg ccc gtc ccc gcc gcg				535
Pro Ala Ala Leu Ala Ala Gln Leu Val Pro Ala Pro Val Pro Ala Ala				
	150	155	160	
gcg ctc cga ccc cgg ccc ccg gtc tac gac gac ggc ccc gcg ggc ccg				583
Ala Leu Arg Pro Arg Pro Pro Val Tyr Asp Asp Gly Pro Ala Gly Pro				
	165	170	175	

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gat gct gag gag gca ggc gac gag aca ccc gac gtg gac ccc gag ctg 631
 Asp Ala Glu Glu Ala Gly Asp Glu Thr Pro Asp Val Asp Pro Glu Leu
 180 185 190
 ttg agg tac ttg ctg gga cgg att ctt gcg gga agc gcg gac tcc gag 679
 Leu Arg Tyr Leu Leu Gly Arg Ile Leu Ala Gly Ser Ala Asp Ser Glu
 195 200 205 210
 ggg gtg gca gcc ccg cgc cgc ctc cgc cgt gcc gcc gac cac gat gtg 727
 Gly Val Ala Ala Pro Arg Arg Leu Arg Arg Ala Ala Asp His Asp Val
 215 220 225
 ggc tct gag ctg ccc cct gag ggc gtg ctg ggg gcg ctg ctg cgt gtg 775
 Gly Ser Glu Leu Pro Pro Glu Gly Val Leu Gly Ala Leu Leu Arg Val
 230 235 240
 aaa cgc cta gag acc ccg gcg ccc cag gtg cct gca cgc cgc ctc ttg 823
 Lys Arg Leu Glu Thr Pro Ala Pro Gln Val Pro Ala Arg Arg Leu Leu
 245 250 255
 cca ccc t gagcactgcc cggatcccggt gcaccctggg acccagaagt gccccgccca 880
 Pro Pro
 260
 tccccccacc aggactgctc cccgccagca cgtccagagc aacttacccc ggccagccag 940
 cccctcacc cgaggatccc taccctctgg ccccaacaata aacatgatct gaagcagc 998

 <210> 121
 <211> 337
 <212> PRT
 <213> Homo sapiens

253/307

<400> 121

Met Thr Ala Gly Gly Gln Ala Glu Ala Glu Gly Ala Gly Gly Glu Pro

1 5 10 15

Gly Ala Ala Arg Leu Pro Ser Arg Val Ala Arg Leu Leu Ser Ala Leu

20 25 30

Phe Tyr Gly Thr Cys Ser Phe Leu Ile Val Leu Val Asn Lys Ala Leu

35 40 45

Leu Thr Thr Tyr Gly Phe Pro Ser Pro Ile Phe Leu Gly Ile Gly Gln

50 55 60

Met Ala Ala Thr Ile Met Ile Leu Tyr Val Ser Lys Leu Asn Lys Ile

65 70 75 80

Ile His Phe Pro Asp Phe Asp Lys Lys Ile Pro Val Lys Leu Phe Pro

85 90 95

Leu Pro Leu Leu Tyr Val Gly Asn His Ile Ser Gly Leu Ser Ser Thr

100 105 110

Ser Lys Leu Ser Leu Pro Met Phe Thr Val Leu Arg Lys Phe Thr Ile

115 120 125

Pro Leu Thr Leu Leu Leu Glu Thr Ile Ile Leu Gly Lys Gln Tyr Ser

130 135 140

Leu Asn Ile Ile Leu Ser Val Phe Ala Ile Ile Leu Gly Ala Phe Ile

145 150 155 160

Ala Ala Gly Ser Asp Leu Ala Phe Asn Leu Glu Gly Tyr Ile Phe Val

165 170 175

Phe Leu Asn Asp Ile Phe Thr Ala Ala Asn Gly Val Tyr Thr Lys Gln

180 185 190

254/307

Lys Met Asp Pro Lys Glu Leu Gly Lys Tyr Gly Val Leu Phe Tyr Asn

195 200 205

Ala Cys Phe Met Ile Ile Pro Thr Leu Ile Ile Ser Val Ser Thr Gly

210 215 220

Asp Leu Gln Gln Ala Thr Glu Phe Asn Gln Trp Lys Asn Val Val Phe

225 230 235 240

Ile Leu Gln Phe Leu Leu Ser Cys Phe Leu Gly Phe Leu Leu Met Tyr

245 250 255

Ser Thr Val Leu Cys Ser Tyr Tyr Asn Ser Ala Leu Thr Thr Ala Val

260 265 270

Val Gly Ala Ile Lys Asn Val Ser Val Ala Tyr Ile Gly Ile Leu Ile

275 280 285

Gly Gly Asp Tyr Ile Phe Ser Leu Leu Asn Phe Val Gly Leu Asn Ile

290 295 300

Cys Met Ala Gly Gly Leu Arg Tyr Ser Phe Leu Thr Leu Ser Ser Gln

305 310 315 320

Leu Lys Pro Lys Pro Val Gly Glu Glu Asn Ile Cys Leu Asp Leu Lys

325 330 335

Ser

<210> 122

<211> 236

<212> PRT

<213> Homo sapiens

255/307

<400> 122

Met Ala Glu Ala Glu Glu Ser Pro Gly Asp Pro Gly Thr Ala Ser Pro

1 5 10 15

Arg Pro Leu Phe Ala Gly Leu Ser Asp Ile Ser Ile Ser Gln Asp Ile

20 25 30

Pro Val Glu Gly Glu Ile Thr Ile Pro Met Arg Ser Arg Ile Arg Glu

35 40 45

Phe Asp Ser Ser Thr Leu Asn Glu Ser Val Arg Asn Thr Ile Met Arg

50 55 60

Asp Leu Lys Ala Val Gly Lys Lys Phe Met His Val Leu Tyr Pro Arg

65 70 75 80

Lys Ser Asn Thr Leu Leu Arg Asp Trp Asp Leu Trp Gly Pro Leu Ile

85 90 95

Leu Cys Val Thr Leu Ala Leu Met Leu Gln Arg Asp Ser Ala Asp Ser

100 105 110

Glu Lys Asp Gly Gly Pro Gln Phe Ala Glu Val Phe Val Ile Val Trp

115 120 125

Phe Gly Ala Val Thr Ile Thr Leu Asn Ser Lys Leu Leu Gly Gly Asn

130 135 140

Ile Ser Phe Phe Gln Ser Leu Cys Val Leu Gly Tyr Cys Ile Leu Pro

145 150 155 160

Leu Thr Val Ala Met Leu Ile Cys Arg Leu Val Leu Leu Ala Asp Pro

165 170 175

Gly Pro Val Asn Phe Met Val Arg Leu Phe Val Val Ile Val Met Phe

180 185 190

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Ala Trp Ser Ile Val Ala Ser Thr Ala Phe Leu Ala Asp Ser Gln Pro

195

200

205

Pro Asn Arg Arg Ala Leu Ala Val Tyr Pro Val Phe Leu Phe Tyr Phe

210

215

220

Val Ile Ser Trp Met Ile Leu Thr Phe Thr Pro Gln

225

230

235

<210> 123

<211> 560

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Ala Pro Ala Glu Ser Leu Arg Arg Arg Lys Thr Gly Tyr Ser

1

5

10

15

Asp Pro Glu Pro Glu Ser Pro Pro Ala Pro Gly Arg Gly Pro Ala Gly

20

25

30

Ser Pro Ala His Leu His Thr Gly Thr Phe Trp Leu Thr Arg Ile Val

35

40

45

Leu Leu Lys Ala Leu Ala Phe Val Tyr Phe Val Ala Phe Leu Val Ala

50

55

60

Phe His Gln Asn Lys Gln Leu Ile Gly Asp Arg Gly Leu Leu Pro Cys

65

70

75

80

Arg Val Phe Leu Lys Asn Phe Gln Gln Tyr Phe Gln Asp Arg Thr Ser

85

90

95

Trp Glu Val Phe Ser Tyr Met Pro Thr Ile Leu Trp Leu Met Asp Trp

257/307

100 105 110
Ser Asp Met Asn Ser Asn Leu Asp Leu Leu Ala Leu Leu Gly Leu Gly
115 120 125
Ile Ser Ser Phe Val Leu Ile Thr Gly Cys Ala Asn Met Leu Leu Met
130 135 140
Ala Ala Leu Trp Gly Leu Tyr Met Ser Leu Val Asn Val Gly His Val
145 150 155 160
Trp Tyr Ser Phe Gly Trp Glu Ser Gln Leu Leu Glu Thr Gly Phe Leu
165 170 175
Gly Ile Phe Leu Cys Pro Leu Trp Thr Leu Ser Arg Leu Pro Gln His
180 185 190
Thr Pro Thr Ser Arg Ile Val Leu Trp Gly Phe Arg Trp Leu Ile Phe
195 200 205
Arg Ile Met Leu Gly Ala Gly Leu Ile Lys Ile Arg Gly Asp Arg Cys
210 215 220
Trp Arg Asp Leu Thr Cys Met Asp Phe His Tyr Glu Thr Gln Pro Met
225 230 235 240
Pro Asn Pro Val Ala Tyr Tyr Leu His His Ser Pro Trp Trp Phe His
245 250 255
Arg Phe Glu Thr Leu Ser Asn His Phe Ile Glu Leu Leu Val Pro Phe
260 265 270
Phe Leu Phe Leu Gly Arg Arg Ala Cys Ile Ile His Gly Val Leu Gln
275 280 285
Ile Leu Phe Gln Ala Val Leu Ile Val Ser Gly Asn Leu Ser Phe Leu
290 295 300

258/307

Asn Trp Leu Thr Met Val Pro Ser Leu Ala Cys Phe Asp Asp Ala Thr
305 310 315 320
Leu Gly Phe Leu Phe Pro Ser Gly Pro Gly Ser Leu Lys Asp Arg Val
325 330 335
Leu Gln Met Gln Arg Asp Ile Arg Gly Ala Arg Pro Glu Pro Arg Phe
340 345 350
Gly Ser Val Val Arg Arg Ala Ala Asn Val Ser Leu Gly Val Leu Leu
355 360 365
Ala Trp Leu Ser Val Pro Val Val Leu Asn Leu Leu Ser Ser Arg Gln
370 375 380
Val Met Asn Thr His Phe Asn Ser Leu His Ile Val Asn Thr Tyr Gly
385 390 395 400
Ala Phe Gly Ser Ile Thr Lys Glu Arg Ala Glu Val Ile Leu Gln Gly
405 410 415
Thr Ala Ser Ser Asn Ala Ser Ala Pro Asp Ala Met Trp Glu Asp Tyr
420 425 430
Glu Phe Lys Cys Lys Pro Gly Asp Pro Ser Arg Arg Pro Cys Leu Ile
435 440 445
Ser Pro Tyr His Tyr Arg Leu Asp Trp Leu Met Trp Phe Ala Ala Phe
450 455 460
Gln Thr Tyr Glu His Asn Asp Trp Ile Ile His Leu Ala Gly Lys Leu
465 470 475 480
Leu Ala Ser Asp Ala Glu Ala Leu Ser Leu Leu Ala His Asn Pro Phe
485 490 495
Ala Gly Arg Pro Pro Pro Arg Trp Val Arg Gly Glu His Tyr Arg Tyr

259/307

500. 505. 510
Lys Phe Ser Arg Pro Gly Gly Arg His Ala Ala Glu Gly Lys Trp Trp
515 520 525
Val Arg Lys Arg Ile Gly Ala Tyr Phe Pro Pro Leu Ser Leu Glu Glu
530 535 540
Leu Arg Pro Tyr Phe Arg Asp Arg Gly Trp Pro Leu Pro Gly Pro Leu
545 550 555 560

<210> 124

<211> 406

<212> PRT

<213> Homo sapiens

<400> 124

Met Ala Glu Asn Gly Lys Asn Cys Asp Gln Arg Arg Val Ala Met Asn

1 5 10 15

Lys Glu His His Asn Gly Asn Phe Thr Asp Pro Ser Ser Val Asn Glu

20 25 30

Lys Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg

35 40 45

Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile

50 55 60

Leu Lys Glu Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val

65 70 75 80

Ser Phe Leu Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu

85 90 95

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Gly Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu

100 105 110

Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly

115 120 125

Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser

130 135 140

Val Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro

145 150 155 160

Pro Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly

165 170 175

Thr Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys

180 185 190

Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met

195 200 205

Ala Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr

210 215 220

Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe

225 230 235 240

Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly

245 250 255

Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp

260 265 270

Leu Ala Gly Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe

275 280 285

Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln

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290 295 300
Lys Ile Phe Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met
305 310 315 320
Val Ala Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys
325 330 335
Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys
340 345 350
Ser Glu Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe
355 360 365
Glu Lys Leu Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile
370 375 380
Asn Ser Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn
385 390 395 400
Ser Glu Glu Lys Thr Lys

405

<210> 125

<211> 453

<212> PRT

<213> Homo sapiens

<400> 125

Met Gly Val Leu Gly Arg Val Leu Leu Trp Leu Gln Leu Cys Ala Leu

1 5 10 15

Thr Gln Ala Val Ser Lys Leu Trp Val Pro Asn Thr Asp Phe Asp Val

20 25 30

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Ala Ala Asn Trp Ser Gln Asn Arg Thr Pro Cys Ala Gly Gly Ala Val

35 40 45

Glu Phe Pro Ala Asp Lys Met Val Ser Val Leu Val Gln Glu Gly His

50 55 60

Ala Val Ser Asp Met Leu Leu Pro Leu Asp Gly Glu Leu Val Leu Ala

65 70 75 80

Ser Gly Ala Gly Phe Gly Val Ser Asp Val Gly Ser His Leu Asp Cys

85 90 95

Gly Ala Gly Glu Pro Ala Val Phe Arg Asp Ser Asp Arg Phe Ser Trp

100 105 110

His Asp Pro His Leu Trp Arg Ser Gly Asp Glu Ala Pro Gly Leu Phe

115 120 125

Phe Val Asp Ala Glu Arg Val Pro Cys Arg His Asp Asp Val Phe Phe

130 135 140

Pro Pro Ser Ala Ser Phe Arg Val Gly Leu Gly Pro Gly Ala Ser Pro

145 150 155 160

Val Arg Val Arg Ser Ile Ser Ala Leu Gly Arg Thr Phe Thr Arg Asp

165 170 175

Glu Asp Leu Ala Val Phe Leu Ala Ser Arg Ala Gly Arg Leu Arg Phe

180 185 190

His Gly Pro Gly Ala Leu Ser Val Gly Pro Glu Asp Cys Ala Asp Pro

195 200 205

Ser Gly Cys Val Cys Gly Asn Ala Glu Ala Gln Pro Trp Ile Cys Ala

210 215 220

Ala Leu Leu Gln Pro Leu Gly Gly Arg Cys Pro Gln Ala Ala Cys His

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225 230 235 240
Ser Ala Leu Arg Pro Gln Gly Gln Cys Cys Asp Leu Cys Gly Ala Val
 245 250 255
Val Leu Leu Thr His Gly Pro Ala Phe Asp Leu Glu Arg Tyr Arg Ala
 260 265 270
Arg Ile Leu Asp Thr Phe Leu Gly Leu Pro Gln Tyr His Gly Leu Gln
 275 280 285
Val Ala Val Ser Lys Val Pro Arg Ser Ser Arg Leu Arg Glu Ala Asp
 290 295 300
Thr Glu Ile Gln Val Val Leu Val Glu Asn Gly Pro Glu Thr Gly Gly
- 305 310 315 320
Ala Gly Arg Leu Ala Arg Ala Leu Leu Ala Asp Val Ala Glu Asn Gly
 325 330 335
Glu Ala Leu Gly Val Leu Glu Ala Thr Met Arg Glu Ser Gly Ala His
 340 345 350
Val Trp Gly Ser Ser Ala Ala Gly Leu Ala Gly Gly Val Ala Ala Ala
 355 360 365
Val Leu Leu Ala Leu Leu Val Leu Leu Val Ala Pro Pro Leu Leu Arg
 370 375 380
Arg Ala Gly Arg Leu Arg Trp Arg Arg His Glu Ala Ala Ala Pro Ala
385 390 395 400
Gly Ala Pro Leu Gly Phe Arg Asn Pro Val Phe Asp Val Thr Ala Ser
 405 410 415
Glu Glu Leu Pro Leu Pro Arg Arg Leu Ser Leu Val Pro Lys Ala Ala
 420 425 430

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Ala Asp Ser Thr Ser His Ser Tyr Phe Val Asn Pro Leu Phe Ala Gly

435

440

445

Ala Glu Ala Glu Ala

450

<210> 126

<211> 59

<212> PRT

<213> Homo sapiens

<400> 126

Met Thr Ser Val Ser Thr Gln Leu Ser Leu Val Leu Met Ser Leu Leu

1

5

10

15

Leu Val Leu Pro Val Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala

20

25

30

Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Cys Ala Cys Leu

35

40

45

Gly Val Tyr Ala Arg Lys Arg Asn Gly Gln Met

50

55

<210> 127

<211> 210

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Leu Pro Gln Met Cys Asp Gly Ser His Leu Ala Ser Thr Leu

265/307

1 5 10 15
Arg Tyr Cys Met Thr Val Ser Gly Thr Val Val Leu Val Ala Gly Thr
20 25 30
Leu Cys Phe Ala Trp Trp Ser Glu Gly Asp Ala Thr Ala Gln Pro Gly
35 40 45
Gln Leu Ala Pro Pro Thr Glu Tyr Pro Val Pro Glu Gly Pro Ser Pro
50 55 60
Leu Leu Arg Ser Val Ser Phe Val Cys Cys Gly Ala Gly Gly Leu Leu
65 70 75 80
Leu Leu Ile Gly Leu Leu Trp Ser Val Lys Ala Ser Ile Pro Gly Pro
85 90 95
Pro Arg Trp Asp Pro Tyr His Leu Ser Arg Asp Leu Tyr Tyr Leu Thr
100 105 110
Val Glu Ser Ser Glu Lys Glu Ser Cys Arg Thr Pro Lys Val Val Asp
115 120 125
Ile Pro Thr Tyr Glu Glu Ala Val Ser Phe Pro Val Ala Glu Gly Pro
130 135 140
Pro Thr Pro Pro Ala Tyr Pro Thr Glu Glu Ala Leu Glu Pro Ser Gly
145 150 155 160
Ser Arg Asp Ala Leu Leu Ser Thr Gln Pro Ala Trp Pro Pro Pro Ser
165 170 175
Tyr Glu Ser Ile Ser Leu Ala Leu Asp Ala Val Ser Ala Glu Thr Thr
180 185 190
Pro Ser Ala Thr Arg Ser Cys Ser Gly Leu Val Gln Thr Ala Arg Gly
195 200 205

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Gly Ser

<210>

<210> 128

<211> 165

<212> PRT

<213> Homo sapiens

<400> 128

Met Asp Ser Ser Arg Ala Arg Gln Gln Leu Arg Arg Arg Phe Leu Leu

1

5

10

15

Leu Pro Asp Ala Glu Ala Gln Leu Asp Arg Glu Gly Asp Ala Gly Pro

20

25

30

Glu Thr Ser Thr Ala Val Glu Lys Lys Glu Lys Pro Leu Pro Arg Leu

35

40

45

Asn Ile His Ser Gly Phe Trp Ile Leu Ala Ser Ile Val Val Thr Tyr

50

55

60

Tyr Val Asp Phe Phe Lys Thr Leu Lys Glu Asn Phe His Thr Ser Ser

65

70

75

80

Trp Phe Leu Cys Gly Ser Ala Leu Leu Leu Val Ser Leu Ser Ile Ala

85

90

95

Phe Tyr Cys Ile Val Tyr Leu Glu Trp Tyr Cys Gly Ile Gly Glu Tyr

100

105

110

Asp Val Lys Tyr Pro Ala Leu Ile Pro Ile Thr Thr Ala Ser Phe Ile

115

120

125

Ala Ala Gly Ile Cys Phe Asn Ile Ala Leu Trp His Val Trp Ser Phe

267/307

130 135 140
Phe Thr Pro Leu Leu Leu Phe Thr Gln Phe Met Gly Val Val Met Phe
145 150 155 160
Ile Thr Leu Leu Gly
165

<210> 129

<211> 162

<212> PRT

<213> Homo sapiens

<400> 129

Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu

1 5 10 15

Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln

20 25 30

Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala

35 40 45

Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe

50 55 60

Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly

65 70 75 80

Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His

85 90 95

Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp

100 105 110

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Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val

115

120

125

Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro

130

135

140

His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val

145

150

155

160

Arg Arg

<210> 130

<211> 221

<212> PRT

<213> Homo sapiens

<400> 130

Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro Ala Cys Gly

1

5

10

15

Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu

20

25

30

Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu

35

40

45

Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro

50

55

60

Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu

65

70

75

80

Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu

85

90

95

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Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile

100

105

110

Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe

115

120

125

Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala

130

135

140

Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp

145

150

155

160

Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly

165

170

175

Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe

180

185

190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr

195

200

205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr

210

215

220

<210> 131

<211> 1011

<212> DNA

<213> Homo sapiens

<400> 131

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ctgccctcgc ggggtggcccgc gctgctgtcg gcgctcttct acgggacctg ctcttccctc 120

atcgtgcttg tcaacaaggc gctgctgacc acctacggtt tcccgtcacc aattttcctt 180

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ggaattggac agatggcagc caccataatg atactatatg tgtccaagct aaacaaaatc 240
attcacttcc ctgattttga taagaaaatt cctgtaaagc tgtttctctc gcctctctc 300
tacgttggaa accacataag tggattatca agcacaagta aattaagcct accgatgttc 360
accgtgctca ggaaattcac cattccactt accttacttc tggaaacat catacttggg 420
aagcagtatt cactcaacat catcctcagt gtctttgcca ttattctcgg ggctttcata 480
gcagctgggt ctgaccttgc ttttaactta gaaggtata tttttgtatt cctgaatgat 540
atcttcacag cagcaaatgg agtttatacc aaacagaaaa tggacccaaa ggagctaggg 600
aaatacggag tacttttcta caatgcctgc ttcattgatta tcccaactct tattattagt 660
gtctccactg gagacctgca acaggctact gaattcaacc aatggaagaa tgttgtgttt 720
atcctacagt ttcttcttct ctgttttttg gggtttctgc tgatgtactc caggttctg 780
tgcagclatt acaattcagc cctgacgaca gcagtgggtg gagccatcaa gaatgtatcc 840
gttgccatac ttgggalatt aatcgggtgga gactacattt tctctttgtt aaactttgla 900
gggttaaata ttgcatggc agggggcttg agatattcct ttttaacact gagcagccag 960
ttaaaacctt aacctgtggg tgaagaaaac atctgtttgg atttgaagag c 1011

<210> 132

<211> 708

<212> DNA

<213> Homo sapiens

<400> 132

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gcaggccctt cagatatatc catctcacia gacatccccg tagaaggaga aatcaccatt 120
cctatgagat ctgcacccg ggagtttgac agctccacat taaatgaatc tgttcgcaat 180
accatcatgc gtgatctaaa agctgttggg aaaaaattca tgcatgtttt gtacccaagg 240
aaaagtaata ctcttttgag agattgggat ttgtggggcc ctttgatcct ttgtgtgaca 300

271/307

ctcgcatataa tgcigcaaag agactctgca gatagtgaag aagatggagg gcccgaattt 360
gcagaggtgt ttgtcattgt ctggttttgt gcagttacca tcacctcaa ctcaaaactt 420
cttggaggga acatatcttt ttttcagagc ctctgtgtgc tgggttactg tataactccc 480
ttgacagtag caatgctgat ttgccggctg gtacttttgg ctgatccagg acctgtaaac 540
ttcatgggtc ggctttttgt ggtgattgtg algtttgcct ggtctatagt tgccctcaca 600
gctttecttg ctgatagcca gcctccaaac cgcagagccc tagctgttta tccgttttcc 660
ctgttttact ttgtcatcag ttggatgatt ctcaccttta ctccctcag 708

<210> 133

<211> 1680

<212> DNA

<213> Homo sapiens

<400> 133

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gaglcgccgc ccgcgccggg gcgtggcccc gcaggtcttc cggcccatct ccacacgggc 120
accttctggc tgaccgggat cgtgctcctg aaggccctag ccttcgtgta cttcgtggca 180
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agagtgttcc tgaagaactt ccagcagtac ttccaggaca ggacgagctg ggaagtcttc 300
agctacatgc ccaccatcct ctggctgalt gactggtcag acatgaactc caacctggac 360
ttgttggttc ttctcggact gggcatctcg tctttcgtac tgatcacggg ctgcgccaac 420
atgcltctca tggttgcctt gtggggcctc tacatgtccc tggtaaatgt gggccatgtc 480
tggtactctt tcggatggga gtcccagctt ctggagacgg ggttccctggg gatcttctg 540
tgccctctgt ggacgtgtc aaggctgccc cagcataccc ccacatcccg gattgtcctg 600
tggggcttcc ggtggctgat cttcaggatc atgcttggag caggccctgat caagatccgg 660
ggggaccggg gctggcgaga cctcaccctg atggacttcc actatgagac ccagccgatg 720

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cccaatcctg tggcatacta cctgcaccac tcaccctggt ggttccatcg cttcgagacg 780
 ctcagcaacc acttcacga gctcctggtg cccttcttcc tcttctcgg ccggcgggcg 840
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 ctcagcttcc tgaactggct gactatggtg ccagccctgg cctgctttga tgacgccacc 960
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 aacgtctcgc tgggcgtcct gctggcctgg ctcagcgtgc ccttggtcct caacttgctg 1140
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 aacgccagcg ccccgatgc catgtgggag gactacgagt tcaagtcaa gccaggtgac 1320
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 ccgccaggt ggttcgagg agagcactac aggtacaagt tcagccgtcc tgggggcagg 1560
 cagccgcgc agggcaagt gtgggtgagg aagaggatcg gacctaact cctccgctc 1620
 agcctggagg agctgaggcc ctacttcagg gaccgtgggt ggcccttgcc cgggcccctc 1680

<210> 134

<211> 1218

<212> DNA

<213> Homo sapiens

<400> 134

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 aatggaaatt tcacagacc ccttcagtg aatgaaaaga agaggaggga gcgggaagaa 120
 aggcagaata ttgtctgtg gagacagccg ctcatcatt tgcagtattt ttctctggaa 180

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atccttgttaa tcttgaagga atggacctca aaattatggc atcgtcaaag catttgtggtg 240
 tctttttttac tgctgcttgc tgtgcttata gctacgtatt atgttgaagg agtgcacaa 300
 cagtatgtgc aacgtataga gaaacagttt cttttgtatg cctactggat aggcttagga 360
 attttgcctt ctgttgggct tggaacaggg ctgcacacct ttctgcttta tctgggtcca 420
 catatagcct cagttacatt agctgcttat gaatgcaatt cagttaattt tcccgaacca 480
 ccctatcctg atcagattat ttgtccagat gaagagggca ctgaaggaac catttctttg 540
 tggagtatca tctcaaaagt taggattgaa gcctgcatgt ggggtatcgg tacagcaatc 600
 ggagagctgc ctccatattt catggccaga gcagctcgcc tctcaggtgc tgaaccagat 660
 gatgaagagt atcaggaatt tgaagagatg ctggaacatg cagagtctgc acaagacttt 720
 gcctcccggt ccaaactggc agttcaaaaa ctagtacaga aagtggatt ttttgggaatt 780
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 atgcatalcc agaaaatttt tglataata acattcagca agcacatagt ggagcaaagt 960
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 tcagaggaga aaactaaa 1218

<210> 135

<211> 1359

<212> DNA

<213> Homo sapiens

<400> 135

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tccaaactct gggccccaa cacggacttc gacgtcgag ccaactggag ccagaaccgg 120
accccggtgc cggcgggcgc cgttgagttc ccggcggaca agatgggtgc agtcctgggt 180
caagaaggtc acgccgtctc agacatgttc ctgccgtgg atggggaact cgtcctgggt 240
tcaggagccg gattcggcgt ctacagcgtg ggctcgacc tggactgtgg cgcgggcgaa 300
cctgccgtct tccgcgactc tgaccgcttc tcctggcatg acccgcacct gtggcgctct 360
ggggacgagg cacctggcct cttcttcgtg gacgccgagc gcgtgccctg ccgccacgac 420
gacgtcttct ttccgcctag tgctctctc cgcgtggggc tcggccctgg cgctagcccc 480
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ggccccgagg actgcgcgga ccgctcgggc tgcgtctgcg gcaacgcgga ggccgagccg 660
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cacggccccg caittgacct ggagcggtac cggcgcgga tactggacac cttctgggt 840
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ggagcgcccc tcggttccg caaccgggtg ttcgacgtga cggcctccga ggagctgccc 1260
ctgcccggc ggctcagct ggttccgaag gcggccgag acagcaccag ccacagttac 1320
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<210> 136

<211> 177

275/307

<212> DNA

<213> Homo sapiens

<400> 136

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atgacctcag ttccaacaca gttgtcctta gtcctcatgt cactgctttt ggtgctgcct    60
gttgtggaag cagtagaagc cggatgatgca atcgcccttt tgtaggtgt ggttctcagc    120
attacaggca tttgtgcctg ctgggggta tatgcacgaa aaagaaatgg acagatg      177
atgacctcag ttccaacaca gttgtcctta gtcctcatgt cactgctttt ggtgctgcct    60
gttgtggaag cagtagaagc cggatgatgca atcgcccttt tgtaggtgt ggttctcagc    120
attacaggca tttgtgcctg ctgggggta tatgcacgaa aaagaaatgg acagatg      177

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<210> 137

<211> 630

<212> DNA

<213> Homo sapiens

<400> 137

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ggggatgcaa cggccagcc tggccagctg gccccacca cggagtatcc ggtgcctgag    180
ggccccagcc cctgctcag gtcgctcagc ttcgtctgct gcggtgcagg tggcctgctg    240
ctgctcattg gcctgctgtg gtcgctcaag gccagcatcc cagggccacc tcgatgggac    300
ccctatcacc tctccagaga cctgtactac ctactgtgg agtcctcaga gaaggagagc    360
tgcaggaccc ccaaagtggg tgacatcccc acttacgagg aagccgtgag cttcccagtg    420
gccgaggggc cccaacacc acctgcatac cctacggagg aagccctgga gccaaagtga    480
tcgagggatg cctgctcag caccagccc gcctggcctc caccagcta tgagagcatc    540
agccttgctc ttgatgccgt ttctgcagag acgacaccga gtgccacag ctctgctca    600

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ggcctgggtc agactgcacg gggaggaagt 630

<210> 138

<211> 495

<212> DNA

<213> Homo sapiens

<400> 138

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gagggccagc tggaccgca gggtagcgc gggccggaaa cctccacagc tgttgagaaa 120

aaggagaaac ctcttccaag acitaaatc cattctggat tctggatttt ggcattccatt 180

gttgtgacct attatgttga cttctttaaa acccttaaag aaaacttcca cactagcagc 240

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gtctacctgg aatggtattg tgggaattgga gaatatgat tcaagtatcc agccttgata 360

cccattacca ctgctcctt tattgcagca ggaatttgct tcaacattgc tttatggcat 420

gtgttggtcgt ttttcactcc attgttgttg tttaaccagt ttatgggggt tgtcatgitt 480

atcacactcc ttgga 495

<210> 139

<211> 486

<212> DNA

<213> Homo sapiens

<400> 139

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ctcttcatca tccaggatat tgcagtcctc ttcaacatca tcatcatitt cctcatgttc 180

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ttcaacacct tegtettcca ggctggcctg gtcaacctcc tattccataa gttcaaaggg 240
 accatcatcc tgacagctgt gtactttgcc ctcagcatct cccctcatgt ctgggtcatg 300
 aacttacgct ggaaaaactc caacagcttc atatggacag atggacttca aatgctgttt 360
 gtattccaga gactagcagc agtgttgtac tgctacttct ataaacggac agccgtaaga 420
 ctaggcgatc ctcacttcta ccaggactct ttgtggctgc gcaaggagtt catgcaagtt 480
 cgaagg 486

<210> 140

<211> 663

<212> DNA

<213> Homo sapiens

<400> 140

atggcggttg cgttggcggc gctggcggcg gtcgagccgg cctgcggcag ccggtaccag 60
 cagttgcaga atgaagaaga gtctggagaa cctgaacagg ctgcaggta tgctcctcca 120
 ccttacagca gcatttctgc agagagcgca gcataatttg actacaagga tgagtctggg 180
 ttccaaagc ccccatctta caatgiagct acaacactgc ccagttatga tgaagcggag 240
 aggaccaagg ctgaagctac tatecccttg gttccctggga gagatgagga ttttgtgggt 300
 cgggatgatt ttgatgatgc tgaccagctg aggataggaa atgatgggat tttcatgtta 360
 acttttttca tggcattcct ctttaactgg attgggtttt tctgtcttt ttgcctgacc 420
 acttcagctg caggaaggta tggggccatt tcaggatttg gtctctctct aattaaatgg 480
 atcctgattg tcaggttttc cacctatttc cctggatatt ttgatggtca gtactggctc 540
 tggltgggtgt tccttgtttt aggccttctc ctgtttctca gaggatttat caattatgca 600
 aaagttcgga agatgccaga aactttctca aatctcccca ggaccagagt tctctttatt 660
 tat 663

278/307

<210> 141

<211> 1622

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (78)...(1091)

<400> 141

ctcttccccg gcccgcccg gcgggaccag tgcgcagccg gggctggcgg gcggcggggt 60

ccgcggggcc gcaggag atg acg gcc ggc ggc cag gcc gag gcc gag ggc 110

Met Thr Ala Gly Gly Gln Ala Glu Ala Glu Gly

1 5 10

gct ggc ggg gag ccc ggc gcg gcg cgg ctg ccc tcg cgg gtg gcc cgg 158

Ala Gly Gly Glu Pro Gly Ala Ala Arg Leu Pro Ser Arg Val Ala Arg

15 20 25

ctg ctg tcg gcg ctc ttc tac ggg acc tgc tcc ttc ctc atc gtg ctt 206

Leu Leu Ser Ala Leu Phe Tyr Gly Thr Cys Ser Phe Leu Ile Val Leu

30 35 40

gtc aac aag gcg ctg ctg acc acc tac ggt ttc ccg tca cca att ttc 254

Val Asn Lys Ala Leu Leu Thr Thr Tyr Gly Phe Pro Ser Pro Ile Phe

45 50 55

ctt gga att gga cag atg gca gcc acc ata atg ata cta tat gtg tcc 302

Leu Gly Ile Gly Gln Met Ala Ala Thr Ile Met Ile Leu Tyr Val Ser

60 65 70 75

aag cta aac aaa atc att cac ttc cct gat ttt gat aag aaa att cct 350

279/307

Lys Leu Asn Lys Ile Ile His Phe Pro Asp Phe Asp Lys Lys Ile Pro
 .80 .85 .90
 gta aag ctg ttt cct ctg cct ctc ctc tac gtt gga aac cac ata agt 398
 Val Lys Leu Phe Pro Leu Pro Leu Leu Tyr Val Gly Asn His Ile Ser
 95 100 105
 gga tta tca agc aca agt aaa tta agc cta ccg atg ttc acc gtg ctc 446
 Gly Leu Ser Ser Thr Ser Lys Leu Ser Leu Pro Met Phe Thr Val Leu
 110 115 120
 agg aaa ttc acc att cca ctt acc tta ctt ctg gaa acc atc ata ctt 494
 Arg Lys Phe Thr Ile Pro Leu Thr Leu Leu Leu Glu Thr Ile Ile Leu
 125 130 135
 ggg aag cag tat tca ctc aac atc atc ctc agt gtc ttt gcc att att 542
 Gly Lys Gln Tyr Ser Leu Asn Ile Ile Leu Ser Val Phe Ala Ile Ile
 140 145 150 155
 ctc ggg gct ttc ata gca gct ggg tct gac ctt gct ttt aac tta gaa 590
 Leu Gly Ala Phe Ile Ala Ala Gly Ser Asp Leu Ala Phe Asn Leu Glu
 160 165 170
 ggc tat att ttt gta ttc ctg aat gat atc ttc aca gca gca aat gga 638
 Gly Tyr Ile Phe Val Phe Leu Asn Asp Ile Phe Thr Ala Ala Asn Gly
 175 180 185
 gtt tat acc aaa cag aaa atg gac cca aag gag cta ggg aaa tac gga 686
 Val Tyr Thr Lys Gln Lys Met Asp Pro Lys Glu Leu Gly Lys Tyr Gly
 190 195 200
 gta ctt ttc tac aat gcc tgc ttc atg att atc cca act ctt att att 734
 Val Leu Phe Tyr Asn Ala Cys Phe Met Ile Ile Pro Thr Leu Ile Ile

280/307

205 210 215
 agt gtc tcc act gga gac ctg caa cag gct act gaa ttc aac caa tgg 782
 Ser Val Ser Thr Gly Asp Leu Gln Gln Ala Thr Glu Phe Asn Gln Trp
 220 225 230 235
 aag aat gtt gtg ttt atc cta cag ttt ctt ctt tcc tgt ttt ttg ggg 830
 Lys Asn Val Val Phe Ile Leu Gln Phe Leu Leu Ser Cys Phe Leu Gly
 240 245 250
 ttt ctg ctg atg tac tcc acg gtt ctg tgc agc tat tac aat tca gcc 878
 Phe Leu Leu Met Tyr Ser Thr Val Leu Cys Ser Tyr Tyr Asn Ser Ala
 255 260 265
 ctg acg aca gca gtg gtt gga gcc atc aag aat gta tcc gtt gcc tac 926
 Leu Thr Thr Ala Val Val Gly Ala Ile Lys Asn Val Ser Val Ala Tyr
 270 275 280
 att ggg ata tta atc ggt gga gac tac att ttc tct ttg tta aac ttt 974
 Ile Gly Ile Leu Ile Gly Gly Asp Tyr Ile Phe Ser Leu Leu Asn Phe
 285 290 295
 gta ggg tta aat att tgc atg gca ggg ggc ttg aga tat tcc ttt tta 1022
 Val Gly Leu Asn Ile Cys Met Ala Gly Gly Leu Arg Tyr Ser Phe Leu
 300 305 310 315
 aca ctg agc agc cag tta aaa cct aaa cct gtg ggt gaa gaa aac atc 1070
 Thr Leu Ser Ser Gln Leu Lys Pro Lys Pro Val Gly Glu Glu Asn Ile
 320 325 330
 tgt ttg gat ttg aag agc ta aagagtctgc agcaggattg gagactgact 1120
 Cys Leu Asp Leu Lys Ser
 335

281/307

tgtgactgcg ggctgggggg gcattcccag taggaatgtg aagccagagg tticggattc 1180
gtgacatcca cccctgggc aagtgagagc atctgcaaaa tgcaaagaga actacctcat 1240
atgcaggatg agccaatggc agtctcaaga aatgtactcg ggcgacacct tacctgtgga 1300
aagcaaalct ttcaaaaata agccactggg actcggtagg tggagcccca gctgctcttc 1360
tagggacctt tggggccctc gtggcatctc tgtgctgtgt gctggggagg aggttgatgt 1420
aatggtgact cttttctgat cagcaccttg gccgtgattc ccaaggtecc agccaaagca 1480
aagggccagt tgtttcagtt taaacagaca tgcttttagt ctaataaaat tagttaactg 1540
ccagtaaagt tattgttag ctttgatgaa agctatgttg gtatctttcc ctaatcatca 1600
aagtaaataa aaaatcattt ct 1622

<210> 142

<211> 2475

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (36)... (746)

<400> 142

acctgtggga ggcacccggg agaaggaggg ccaag atg gcg gaa gcg gag gag 53

Met Ala Glu Ala Glu Glu

1 5

tct cca gga gac ccg ggg aca gca tcg ccc agg ccc ctg ttt gca ggc 101

Ser Pro Gly Asp Pro Gly Thr Ala Ser Pro Arg Pro Leu Phe Ala Gly

10 15 20

ctt tca gat ala tcc atc tca caa gac atc ccc gta gaa gga gaa atc 149

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Leu Ser Asp Ile Ser Ile Ser Gln Asp Ile Pro Val Glu Gly Glu Ile
 25 30 35
 acc att cct atg aga tct cgc atc cgg gag ttt gac agc tcc aca tta 197
 Thr Ile Pro Met Arg Ser Arg Ile Arg Glu Phe Asp Ser Ser Thr Leu
 40 45 50
 aat gaa tct gtt cgc aat acc atc atg cgt gat cta aaa gct gtt ggg 245
 Asn Glu Ser Val Arg Asn Thr Ile Met Arg Asp Leu Lys Ala Val Gly
 55 60 65 70
 aaa aaa ttc atg cat gtt ttg tac cca agg aaa agt aat act ctt ttg 293
 Lys Lys Phe Met His Val Leu Tyr Pro Arg Lys Ser Asn Thr Leu Leu
 75 80 85
 aga gat tgg gat ttg tgg ggc cct ttg atc ctt tgt gtg aca ctc gca 341
 Arg Asp Trp Asp Leu Trp Gly Pro Leu Ile Leu Cys Val Thr Leu Ala
 90 95 100
 tta atg ctg caa aga gac tct gca gat agt gaa aaa gat gga ggg ccc 389
 Leu Met Leu Gln Arg Asp Ser Ala Asp Ser Glu Lys Asp Gly Gly Pro
 105 110 115
 caa ttt gca gag gtg ttt gtc att gtc tgg ttt ggt gca gtt acc atc 437
 Gln Phe Ala Glu Val Phe Val Ile Val Trp Phe Gly Ala Val Thr Ile
 120 125 130
 acc ctc aac tca aaa ctt ctt gga ggg aac ata tct ttt ttt cag agc 485
 Thr Leu Asn Ser Lys Leu Leu Gly Gly Asn Ile Ser Phe Phe Gln Ser
 135 140 145 150
 ctc tgt gtg ctg ggt tac tgt ata ctt ccc ttg aca gta gca atg ctg 533
 Leu Cys Val Leu Gly Tyr Cys Ile Leu Pro Leu Thr Val Ala Met Leu

283/307

155	160	165	
att tgc cgg ctg gta ctt ttg gct gat cca gga cct gta aac ttc atg			581
Ile Cys Arg Leu Val Leu Leu Ala Asp Pro Gly Pro Val Asn Phe Met			
170	175	180	
gtt cgg ctt ttt gtg gtg att gtg atg ttt gcc tgg tct ata gtt gcc			629
Val Arg Leu Phe Val Val Ile Val Met Phe Ala Trp Ser Ile Val Ala			
185	190	195	
tcc aca gct ttc ctt gct gat agc cag cct cca aac cgc aga gcc cta			677
Ser Thr Ala Phe Leu Ala Asp Ser Gln Pro Pro Asn Arg Arg Ala Leu			
200	205	210	
gct gtt tat cct gtt ttc ctg ttt tac ttt gtc atc agt tgg atg att			725
Ala Val Tyr Pro Val Phe Leu Phe Tyr Phe Val Ile Ser Trp Met Ile			
215	220	225	230
ctc acc ttt act cct cag taaatca ggaatgggaa attaaaaacc agtgaattga			780
Leu Thr Phe Thr Pro Gln			
235			
aagcacatct gaaagatgca attcaccatg gagctttgtc tctggccctt atttgtctaa			840
ttttggaggt atttgataac tgagtaggtg aggagattaa aaggagacca tatagcactg			900
tcacccctta tttaggaac tgatgtttga aaggctgttc tttctctct taatgtcatt			960
tcttlaaaaa tacatgtgca taclacacac agtatataat gcctccttaa ggcatgatgg			1020
agtcaccgtg gtccatttgg gtgacaacca glgacttggg aagcacatag atacatctta			1080
caagttgaat agagttgata actattttca gttttgagaa taccagttca ggtgcagctc			1140
ttaaacacat tgccttatga ctattagaat atgcctctct tttcataaat aaaaatacat			1200
ggtctatata cttttcttt tttttctctc tcttaagctt aaaaaggcaa tgagagaggt			1260
taggagtggg ttcalacacg gagaatgaga aaacatgcat taaccaatat tcagattttg			1320

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atcaggggaa attctacact tgttgcaaaa aaaaaaaaaa aaaaagcaaa gggcctctaa 1380
 agaatcagcc tctttgggtcc ctttgtgtg tcaccttttt gccatgttta acagcatctt 1440
 ggttggcact ctagtcttaa tcttgctcct taactttgaa tatgcagtct aaaatgtcag 1500
 tagtcaacat gtaattttcc tttgaaattc tgaatattcc agtgctggaa cttatccaaa 1560
 aagaagacct cagaaactta gattggtaga tctctagtgc atattatcat gtgggcacct 1620
 tctcttaggg tggaatgagg cagtctgga gcagcatagt taaaaggagc tgtttaatat 1680
 tctctgtagt ctggcctctt aactagaaag taaagctaaa tcagaagcct gtatttaacc 1740
 atgtgaacag ggagggattt agtgttctga tggctgatta atagaacagc tagatactta 1800
 gagcatgacg tgggatggga tgagtttaca gctgctgcct tttcatggtg agcttagcag 1860
 ttttctcatt agaigtgttt ttttgggttg gggaatagca atttatttta ttgattttag 1920
 actttatcaa gctaattagc tcccccttag ataagtacat gttgcacatg tgcacctact 1980
 tgtaatctca galattttatg cacacaagtg tgaaggtttt tcaggagca gagcatctgg 2040
 gacaggctga tcttgagcta aacagggtc ctttaaggca atatgaactg ttgccttcta 2100
 taaattgcac attgaggaac tctaatagac aaagattagg tgtcaggcag aaaacactca 2160
 ttgtaaatat actattagtt gataaacata ggactttctt attccccagt ttttctttat 2220
 calataattt aaatatttat tcattttgta tttaaagact acctacacat agatatatga 2280
 ttccaaagtc atactttctc catccccaca ttagccaagt gaatacagg ccaaatgggt 2340
 tcttggaatg ataataacaa agcattacaa agtgggtccc cttggttcca gccttgtcca 2400
 gagtttttgg ttatatattt ctatttatta caatttacct tttaaattgt aaaataaacc 2460
 tttgtgtgga cagag 2475

<210> 143

<211> 1739

<212> DNA

<213> Homo sapiens

285/307

<220>

<221> CDS

<222> (21)... (1703)

<400>..143

tgcgccctga cagcccaaca atg gcg gcg ccc gcg gag tcg ctg agg agg 50

Met Ala Ala Pro Ala Glu Ser Leu Arg Arg

1 5 10

cgg aag act ggg tac tcg gat ccg gag cct gag tcg ccg ccc gcg ccg 98

Arg Lys Thr Gly Tyr Ser Asp Pro Glu Pro Glu Ser Pro Pro Ala Pro

15 20 25

ggg cgt ggc ccc gca ggc tct ccg gcc cat ctc cac acg ggc acc ttc 146

Gly Arg Gly Pro Ala Gly Ser Pro Ala His Leu His Thr Gly Thr Phe

30 35 40

tgg ctg acc cgg atc gtg ctc ctg aag gcc cta gcc ttc gtg tac ttc 194

Trp Leu Thr Arg Ile Val Leu Leu Lys Ala Leu Ala Phe Val Tyr Phe

45 50 55

gtg gca ttc ctg gtg gct ttc cat cag aac aag cag ctc atc ggt gac 242

Val Ala Phe Leu Val Ala Phe His Gln Asn Lys Gln Leu Ile Gly Asp

60 65 70

agg ggg ctg ctt ccc tgc aga gtg ttc ctg aag aac ttc cag cag tac 290

Arg Gly Leu Leu Pro Cys Arg Val Phe Leu Lys Asn Phe Gln Gln Tyr

75 80 85 90

ttc cag gac agg acg agc tgg gaa gtc ttc agc tac atg ccc acc atc 338

Phe Gln Asp Arg Thr Ser Trp Glu Val Phe Ser Tyr Met Pro Thr Ile

95 100 105

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ctc tgg ctg atg gac tgg tca gac atg aac tcc aac ctg gac ttg ctg 386

Leu Trp Leu Met Asp Trp Ser Asp Met Asn Ser Asn Leu Asp Leu Leu

110

115

120

gct ctt ctc gga ctg ggc atc tcg tct ttc gta ctg atc acg ggc tgc 434

Ala Leu Leu Gly Leu Gly Ile Ser Ser Phe Val Leu Ile Thr Gly Cys

125

130

135

gcc aac atg ctt ctc atg gct gcc ctg tgg ggc ctc tac atg tcc ctg 482

Ala Asn Met Leu Leu Met Ala Ala Leu Trp Gly Leu Tyr Met Ser Leu

140

145

150

gtt aat gtg ggc cat gtc tgg tac tct ttc gga tgg gag tcc cag ctt 530

Val Asn Val Gly His Val Trp Tyr Ser Phe Gly Trp Glu Ser Gln Leu

155

160

165

170

ctg gag acg ggg ttc ctg ggg atc ttc ctg tgc cct ctg tgg acg ctg 578

Leu Glu Thr Gly Phe Leu Gly Ile Phe Leu Cys Pro Leu Trp Thr Leu

175

180

185

tca agg ctg ccc cag cat acc ccc aca tcc cgg att gtc ctg tgg ggc 626

Ser Arg Leu Pro Gln His Thr Pro Thr Ser Arg Ile Val Leu Trp Gly

190

195

200

ttc cgg tgg ctg atc ttc agg atc atg ctt gga gca ggc ctg atc aag 674

Phe Arg Trp Leu Ile Phe Arg Ile Met Leu Gly Ala Gly Leu Ile Lys

205

210

215

atc cgg ggg gac cgg tgc tgg cga gac ctc acc tgc atg gac ttc cac 722

Ile Arg Gly Asp Arg Cys Trp Arg Asp Leu Thr Cys Met Asp Phe His

220

225

230

tat gag acc cag ccg atg ccc aat cct gtg gca tac tac ctg cac cac 770

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Tyr Glu Thr Gln Pro Met Pro Asn Pro Val Ala Tyr Tyr Leu His His
 235 240 245 250
 tca ccc tgg tgg ttc cat cgc ttc gag acg ctc agc aac cac ttc atc 818
 Ser Pro Trp Trp Phe His Arg Phe Glu Thr Leu Ser Asn His Phe Ile
 255 260 265
 gag ctc ctg gtg ccc ttc ttc ctc ttc ctc ggc cgg cgg gcg tgc atc 866
 Glu Leu Leu Val Pro Phe Phe Leu Phe Leu Gly Arg Arg Ala Cys Ile
 270 275 280
 atc cac ggg gtg ctg cag atc ctg ttc cag gcc gtc ctc atc gtc agc 914
 Ile His Gly Val Leu Gln Ile Leu Phe Gln Ala Val Leu Ile Val Ser
 285 290 295
 ggg aac ctc agc ttc ctg aac tgg ctg act atg gtg ccc agc ctg gcc 962
 Gly Asn Leu Ser Phe Leu Asn Trp Leu Thr Met Val Pro Ser Leu Ala
 300 305 310
 tgc ttt gat gac gcc acc ctg gga ttc ttg ttc ccc tct ggg cca ggc 1010
 Cys Phe Asp Asp Ala Thr Leu Gly Phe Leu Phe Pro Ser Gly Pro Gly
 315 320 325 330
 agc ctg aag gac cga gtt ctg cag atg cag agg gac atc cga ggg gcc 1058
 Ser Leu Lys Asp Arg Val Leu Gln Met Gln Arg Asp Ile Arg Gly Ala
 335 340 345
 cgg ccc gag ccc aga ttc ggc tcc gtg gtg cgg cgt gca gcc aac gtc 1106
 Arg Pro Glu Pro Arg Phe Gly Ser Val Val Arg Arg Ala Ala Asn Val
 350 355 360
 tcg ctg ggc gtc ctg ctg gcc tgg ctc agc gtg ccc gtg gtc ctc aac 1154
 Ser Leu Gly Val Leu Leu Ala Trp Leu Ser Val Pro Val Val Leu Asn

288/307

365 370 375
ttg ctg agc tcc agg cag gtc atg aac acc cac ttc aac tct ctt cac 1202
Leu Leu Ser Ser Arg Gln Val Met Asn Thr His Phe Asn Ser Leu His
380 385 390
atc gtc aac act tac ggg gcc ttc gga agc atc acc aag gag cgg gcg 1250
Ile Val Asn Thr Tyr Gly Ala Phe Gly Ser Ile Thr Lys Glu Arg Ala
395 400 405 410
gag gtg atc ctg cag ggc aca gcc agc tcc aac gcc agc gcc ccc gat 1298
Glu Val Ile Leu Gln Gly Thr Ala Ser Ser Asn Ala Ser Ala Pro Asp
415 420 425
gcc atg tgg gag gac tac gag ttc aag tgc aag cca ggt gac ccc agc 1346
Ala Met Trp Glu Asp Tyr Glu Phe Lys Cys Lys Pro Gly Asp Pro Ser
430 435 440
aga cgg ccc tgc ctc atc tcc ccg tac cac tac cgc ctg gac tgg ctg 1394
Arg Arg Pro Cys Leu Ile Ser Pro Tyr His Tyr Arg Leu Asp Trp Leu
445 450 455
atg tgg ttc gcg gcc ttc cag acc tac gag cac aac gac tgg atc atc 1442
Met Trp Phe Ala Ala Phe Gln Thr Tyr Glu His Asn Asp Trp Ile Ile
460 465 470
cac ctg gct ggc aag ctc ctg gcc agc gac gcc gag gcc ttg tcc ctg 1490
His Leu Ala Gly Lys Leu Leu Ala Ser Asp Ala Glu Ala Leu Ser Leu
475 480 485 490
ctg gca cac aac ccc ttc gcg ggc agg ccc ccg ccc agg tgg gtc cga 1538
Leu Ala His Asn Pro Phe Ala Gly Arg Pro Pro Pro Arg Trp Val Arg
495 500 505

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gga gag cac tac agg tac aag ttc agc cgt cct ggg ggc agg cac gcc 1586

Gly Glu His Tyr Arg Tyr Lys Phe Ser Arg Pro Gly Gly Arg His Ala

510

515

520

gcc gag ggc aag tgg tgg gtg cgg aag agg atc gga gcc tac ttc cct 1634

Ala Glu Gly Lys Trp Trp Val Arg Lys Arg Ile Gly Ala Tyr Phe Pro

525

530

535

ccg ctc agc ctg gag gag ctg agg ccc tac ttc agg gac cgt ggg tgg 1682

Pro Leu Ser Leu Glu Glu Leu Arg Pro Tyr Phe Arg Asp Arg Gly Trp

540

545

550

cct ctg ccc ggg ccc ctc tagacgtgca ccagaaataa aggccaagac 1730

Pro Leu Pro Gly Pro Leu

555

560

ccagccccc

1739

<210> 144

<211> 2005

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (107)... (1327)

<400> 144

ggagcccagc ggcgggtgtg agagtccgta aggagcagct tccaggatcc tgaatccgg 60

agcagccggg gtcggagcgg ctctcaaga gttactgac tatgaa atg gca gag 115

Met Ala Glu

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aat gga aaa aat tgt gac cag aga cgt gta gca atg aac aag gaa cat : 163
 Asn Gly Lys Asn Cys Asp Gln Arg Arg Val Ala Met Asn Lys Glu His

5 10 15

cat aat gga aat ttc aca gac ccc tct tca gtg aat gaa aag aag agg : 211
 His Asn Gly Asn Phe Thr Asp Pro Ser Ser Val Asn Glu Lys Lys Arg

20 25 30 35

agg gag cgg gaa gaa agg cag aat att gtc ctg tgg aga cag ccg ctc : 259
 Arg Glu Arg Glu Glu Arg Gln Asn Ile Val Leu Trp Arg Gln Pro Leu

40 45 50

att acc ttg cag tat ttt tct ctg gaa atc ctt gta atc ttg aag gaa : 307
 Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile Leu Val Ile Leu Lys Glu

55 60 65

tgg acc tca aaa tta tgg cat cgt caa agc att gtg gtg tct ttt tta : 355
 Trp Thr Ser Lys Leu Trp His Arg Gln Ser Ile Val Val Ser Phe Leu

70 75 80

ctg ctg ctt gct gtg ctt ata gct acg tat tat gtt gaa gga gtg cat : 403
 Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr Tyr Val Glu Gly Val His

85 90 95

caa cag tat gtg caa cgt ata gag aaa cag ttt ctt ttg tat gcc tac : 451
 Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln Phe Leu Leu Tyr Ala Tyr

100 105 110 115

tgg ata ggc tta gga att ttg tct tct gtt ggg ctt gga aca ggg ctg : 499
 Trp Ile Gly Leu Gly Ile Leu Ser Ser Val Gly Leu Gly Thr Gly Leu

120 125 130

291/307

cac acc ttt ctg ctt tat ctg ggt cca cat ata gcc tca gtt aca tta 547
His Thr Phe Leu Leu Tyr Leu Gly Pro His Ile Ala Ser Val Thr Leu
135 140 145
gct gct tat gaa tgc aat tca gtt aat ttt ccc gaa cca ccc tat cct 595
Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe Pro Glu Pro Pro Tyr Pro
150 155 160
gat cag att att tgt cca gat gaa gag ggc act gaa gga acc att tct 643
Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly Thr Glu Gly Thr Ile Ser
165 170 175
ttg tgg agt atc atc tca aaa gtt agg att gaa gcc tgc atg tgg ggt 691
Leu Trp Ser Ile Ile Ser Lys Val Arg Ile Glu Ala Cys Met Trp Gly
180 185 190 195
atc ggt aca gca atc gga gag ctg cct cca tat ttc atg gcc aga gca 739
Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro Tyr Phe Met Ala Arg Ala
200 205 210
gct cgc ctc tca ggt gct gaa cca gat gat gaa gag tat cag gaa ttt 787
Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp Glu Glu Tyr Gln Glu Phe
215 220 225
gaa gag atg ctg gaa cat gca gag tct gca caa gac ttt gcc tcc cgg 835
Glu Glu Met Leu Glu His Ala Glu Ser Ala Gln Asp Phe Ala Ser Arg
230 235 240
gcc aaa ctg gca gtt caa aaa cta gta cag aaa gtt gga ttt ttt gga 883
Ala Lys Leu Ala Val Gln Lys Leu Val Gln Lys Val Gly Phe Phe Gly
245 250 255
att ttg gcc tgt gct tca att cca aat cct tta ttt gat ctg gct gga 931

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Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro Leu Phe Asp Leu Ala Gly
 260 265 270 275
 ata acg tgt gga cac ttt ctg gta cct ttt tgg acc ttc ttt ggt gca 979
 Ile Thr Cys Gly His Phe Leu Val Pro Phe Trp Thr Phe Phe Gly Ala
 280 285 290
 acc cta att gga aaa gca ata ata aaa atg cat atc cag aaa att ttt 1027
 Thr Leu Ile Gly Lys Ala Ile Ile Lys Met His Ile Gln Lys Ile Phe
 295 300 305
 gtt ata ata aca ttc agc aag cac ata gtg gag caa atg gtg gct ttc 1075
 Val Ile Ile Thr Phe Ser Lys His Ile Val Glu Gln Met Val Ala Phe
 310 315 320
 att ggt gct gtc ccc ggc ata ggt cca tct ctg cag aag cca ttt cag 1123
 Ile Gly Ala Val Pro Gly Ile Gly Pro Ser Leu Gln Lys Pro Phe Gln
 325 330 335
 gag tac ctg gag gct caa cgg cag aag ctt cac cac aaa agc gaa atg 1171
 Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu His His Lys Ser Glu Met
 340 345 350 355
 ggc aca cca cag gga gaa aac tgg ttg tcc tgg atg ttt gaa aag ttg 1219
 Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser Trp Met Phe Glu Lys Leu
 360 365 370
 gtc gtt gtc atg gtg tgt tac ttc atc cta tct atc att aac tcc atg 1267
 Val Val Val Met Val Cys Tyr Phe Ile Leu Ser Ile Ile Asn Ser Met
 375 380 385
 gca caa agt tat gcc aaa cga atc cag cag cgg ttg aac tca gag gag 1315
 Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln Arg Leu Asn Ser Glu Glu

293/307

390

395

400

aaa act aaa taagta gagaaagttt taaactgcag aaattggagt ggatgggttc 1370

Lys Thr Lys

405

tgccttaaat tgggaggact ccaagccggg aaggaaaatt cccttttcca acctgtatca 1430

atttttacaa cttttttcct gaaagcagtt tagtccatac ttgactga catacttttt 1490

ccctctgtgc taaggtaagg tatccaccct cgatgcaatc caccttgtgt ttcttaggg 1550

tggaatgtga tgttcagcag caaacttgca acagactggc cttctgtttg ttactttcaa 1610

aaggcccaca tgatacaatt agagaattcc caccgcacaa aaaaagttcc taagtatgtt 1670

aaatatgtca agcttttttag gcttgcaca aatgattgct ttgttttcct aagtcacaa 1730

aatgtatata aattatctag atgggalaac agtcttgcat gtttatcatg ttacaattta 1790

atatccatc ctgcccaccc ctccctctcc catcctcaaa aaagggccat ttatgatgc 1850

attgcacacc ctctggggaa attgatcttt aaattttgag acagtataag gaaaatctgg 1910

ttgggtgtctt acaagtgagc tgacaccatt ttttattctg tgtatttaga atgaagtctt 1970

gaaaaaaact ttataaagac atctttaatc attcc 2005

<210> 145

<211> 1558

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (31)... (1392)

<400> 145

tcccggtcgg,gtgcaaggag ccgaggcgag atg ggc gtc ctg ggc cgg gtc ctg 54

294/307

Met Gly Val Leu Gly Arg Val Leu

1

5

ctg tgg ctg cag ctc tgc gca ctg acc cag gcg gtc tcc aaa ctc tgg 102

Leu Trp Leu Gln Leu Cys Ala Leu Thr Gln Ala Val Ser Lys Leu Trp

10

15

20

gtc ccc aac acg gac ttc gac gtc gca gcc aac tgg agc cag aac cgg 150

Val Pro Asn Thr Asp Phe Asp Val Ala Ala Asn Trp Ser Gln Asn Arg

25

30

35

40

acc ccg tgc gcc ggc ggc gcc gtt gag ttc ccg gcg gac aag atg gtg 198

Thr Pro Cys Ala Gly Gly Ala Val Glu Phe Pro Ala Asp Lys Met Val

45

50

55

tca gtc ctg gtg caa gaa ggt cac gcc gtc tca gac atg ctc ctg ccg 246

Ser Val Leu Val Gln Glu Gly His Ala Val Ser Asp Met Leu Leu Pro

60

65

70

ctg gat ggg gaa ctc gtc ctg gct tca gga gcc gga ttc ggc gtc tca 294

Leu Asp Gly Glu Leu Val Leu Ala Ser Gly Ala Gly Phe Gly Val Ser

75

80

85

gac gtg ggc tgc cac ctg gac tgt ggc gcg ggc gaa cct gcc gtc ttc 342

Asp Val Gly Ser His Leu Asp Cys Gly Ala Gly Glu Pro Ala Val Phe

90

95

100

cgc gac tct gac cgc ttc tcc tgg cat gac ccg cac ctg tgg cgc tct 390

Arg Asp Ser Asp Arg Phe Ser Trp His Asp Pro His Leu Trp Arg Ser

105

110

115

120

ggg gac gag gca cct ggc ctc ttc ttc gtg gac gcc gag cgc gtg ccc 438

Gly Asp Glu Ala Pro Gly Leu Phe Phe Val Asp Ala Glu Arg Val Pro

295/307

125	130	135	
tgc cgc cac gac gac gtc ttc ttt ccg cct agt gcc tcc ttc cgc gtg			486
Cys Arg His Asp Asp Val Phe Phe Pro Pro Ser Ala Ser Phe Arg Val			
140	145	150	
ggg ctc ggc cct ggc gct agc ccc gtg cgt gtc cgc agc atc tcg gct			534
Gly Leu Gly Pro Gly Ala Ser Pro Val Arg Val Arg Ser Ile Ser Ala			
155	160	165	
ctg ggc cgg acg ttc acg cgc gac gag gac ctg gct gtt ttc ctg gcg			582
Leu Gly Arg Thr Phe Thr Arg Asp Glu Asp Leu Ala Val Phe Leu Ala			
170	175	180	
tcc cgc gcg ggc cgc cta cgc ttc cac ggg ccg ggc gcg ctg agc gtg			630
Ser Arg Ala Gly Arg Leu Arg Phe His Gly Pro Gly Ala Leu Ser Val			
185	190	195	200
ggc ccc gag gac tgc gcg gac ccg tcg ggc tgc gtc tgc ggc aac gcg			678
Gly Pro Glu Asp Cys Ala Asp Pro Ser Gly Cys Val Cys Gly Asn Ala			
205	210	215	
gag gcg cag ccg tgg atc tgc gcg gcc ctg ctc cag ccc ctg ggc ggc			726
Glu Ala Gln Pro Trp Ile Cys Ala Ala Leu Leu Gln Pro Leu Gly Gly			
220	225	230	
cgc tgc ccc cag gcc gcc tgc cac agc gcc ctc cgg ccc cag ggg cag			774
Arg Cys Pro Gln Ala Ala Cys His Ser Ala Leu Arg Pro Gln Gly Gln			
235	240	245	
tgc tgt gac ctc tgt gga gcc gtt gtg ttg ctg acc cac ggc ccc gca			822
Cys Cys Asp Leu Cys Gly Ala Val Val Leu Leu Thr His Gly Pro Ala			
250	255	260	

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ttt gac ctg gag cgg tac cgg gcg cgg ata ctg gac acc ttc ctg ggt 870

Phe Asp Leu Glu Arg Tyr Arg Ala Arg Ile Leu Asp Thr Phe Leu Gly

265 270 275 280

ctg cct cag tac cac ggg ctg cag gtg gcc gtg tcc aag gtg cca cgc 918

Leu Pro Gln Tyr His Gly Leu Gln Val Ala Val Ser Lys Val Pro Arg

285 290 295

tcg tcc cgg ctc cgt gag gcc gat acg gag atc cag gtg gtg ctg gtg 966

Ser Ser Arg Leu Arg Glu Ala Asp Thr Glu Ile Gln Val Val Leu Val

300 305 310

gag aat ggg ccc gag aca ggc gga gcg ggg cgg ctg gcc cgg gcc ctc 1014

Glu Asn Gly Pro Glu Thr Gly Gly Ala Gly Arg Leu Ala Arg Ala Leu

315 320 325

ctg gcg gac gtc gcc gag aac ggc gag gcc ctc ggc gtc ctg gag gcg 1062

Leu Ala Asp Val Ala Glu Asn Gly Glu Ala Leu Gly Val Leu Glu Ala

330 335 340

acc atg cgg gag tcg ggc gca cac gtc tgg ggc agc tcc gcg gct ggg 1110

Thr Met Arg Glu Ser Gly Ala His Val Trp Gly Ser Ser Ala Ala Gly

345 350 355 360

ctg gcg ggc ggc gtg gcg gct gcc gtg ctg ctg gcg ctg ctg gtc ctg 1158

Leu Ala Gly Gly Val Ala Ala Ala Val Leu Leu Ala Leu Leu Val Leu

365 370 375

ctg gtg gcg ccg ccg ctg ctg cgc cgc gcg ggg agg ctc agg tgg agg 1206

Leu Val Ala Pro Pro Leu Leu Arg Arg Ala Gly Arg Leu Arg Trp Arg

380 385 390

agg cac gag gcg gcg gcc ccg gct gga gcg ccc ctc ggc ttc cgc aac 1254

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Arg His Glu Ala Ala Ala Pro Ala Gly Ala Pro Leu Gly Phe Arg Asn

395

400

405

ccg gtg ttc gac gtg acg gcc tcc gag gag ctg ccc ctg ccg cgg cgg 1302

Pro Val Phe Asp Val Thr Ala Ser Glu Glu Leu Pro Leu Pro Arg Arg

410

415

420

ctc agc ctg gtt ccg aag gcg gcc gca gac agc acc agc cac agt tac 1350

Leu Ser Leu Val Pro Lys Ala Ala Ala Asp Ser Thr Ser His Ser Tyr

425

430

435

440

ttc gtc aac cct ctg ttc gcc ggg gcc gag gcc gag gcc t gagcggccgc 1400

Phe Val Asn Pro Leu Phe Ala Gly Ala Glu Ala Glu Ala

445

450

ctgaccgtcg accttggggc tctccacccc ctctggcccc agtcgaactg. ggggctagcc 1460

acctctctgt ccagccccca aacctcccct tcttttcccc ctctctccggg ggccaaggac 1520

agggtggcct tactcagtaa aggtgtttcc tgcacctg 1558

<210> 146

<211> 1005

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (151)... (330)

<400> 146

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ccggagctcc aggaaggga aatttcaagt cagatagaat tctatatata ccatttcttt 120

298/307

ggaaccttca gccctcaaga ttccaacatc atg acc tca gtt tca aca cag ttg 174

Met Thr Ser Val Ser Thr Gln Leu

1

5

tcc tta gtc ctc atg tca ctg ctt ttg gtg ctg cct gtt gtg gaa gca 222

Ser Leu Val Leu Met Ser Leu Leu Leu Val Leu Pro Val Val Glu Ala

10

15

20

gta gaa gcc ggt gat gca atc gcc ctt ttg tta ggt gtg gtt ctc agc 270

Val Glu Ala Gly Asp Ala Ile Ala Leu Leu Leu Gly Val Val Leu Ser

25

30

35

40

att aca ggc att tgt gcc tgc ttg ggg gla tat gca cga aaa aga aat 318

Ile Thr Gly Ile Cys Ala Cys Leu Gly Val Tyr Ala Arg Lys Arg Asn

45

50

55

gga cag atg tga ctttgaaagg cctactgagt caaacctcac cctgaaaacc 370

Gly Gln Met

tttgcgcttt agaggctaaa cctgagattt ggtglgtgaa aggttccaag aatcagtaaa 430

taaggagatt tcacattttt catlgtttcc atgaaatggc aacaaacata cattataaaa 490

ttgaaaaaaa aatgttttct ttacaacaaa taalgcacag aaaaatgcag cctataattt 550

gclagtlagg tagtcaaaga agtaagatgg ctgaaattta cataagtaat atttcataat 610

cttagaattc tctcaaagca tgtgaaatag gaagaaggaa gtctcttgccc agaattcttag 670

gaaatcacca ctgttcggtt ataactactg cctcctgaat cgttgaggag tctttttaa 730

tagatttttg ttttgttgc tccaagtta atattatatt tagatatcag agagtcaggc 790

aaaaaggaaa acttttatct ctagggaaaa aacatttaga aaaatgtatt cagtgtatct 850

aatacigaaa tgcggaaaaa aatttaatgt taaaaaaaa actatagaca ttgacatgga 910

aaagagattt aatgttttga aaaaaaactt tatattaact gagtaacatc ctccctgatga 970

gaagtactat attaaalata aaccatttat gttat 1005

299/307

<210> 147

<211> 969

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (151)... (783)

<400> 147

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ggtcgctcag cctgcccgtc cttcaccacc acaccttcac ctgcgccag ctccctgcgc 120

gcctggacag cgctgctgc ccgcctcccg atg gcc ctg ccc cag atg tgt gac 174

Met Ala Leu Pro Gln Met Cys Asp

1

5

ggg agc cac ttg gcc tcc acc ctc cgc tat tgc atg aca gtc agc ggc 222

Gly Ser His Leu Ala Ser Thr Leu Arg Tyr Cys Met Thr Val Ser Gly

10

15

20

aca gtg gtt ctg gtg gcc ggg acg ctc tgc ttc gct tgg tgg agc gaa 270

Thr Val Val Leu Val Ala Gly Thr Leu Cys Phe Ala Trp Trp Ser Glu

25

30

35

40

ggg gat gca acc gcc cag cct ggc cag ctg gcc cca ccc acg gag tat 318

Gly Asp Ala Thr Ala Gln Pro Gly Gln Leu Ala Pro Pro Thr Glu Tyr

45

50

55

ccg gtg cct gag ggc ccc agc ccc ctg ctc agg tcc gtc agc ttc gtc 366

Pro Val Pro Glu Gly Pro Ser Pro Leu Leu Arg Ser Val Ser Phe Val

300/307

60	65	70	
tgc tgc ggt gca ggt ggc ctg ctg ctg ctc att ggc ctg ctg tgg tcc			414
Cys Cys Gly Ala Gly Gly Leu Leu Leu Leu Ile Gly Leu Leu Trp Ser			
75	80	85	
gtc aag gcc agc atc cca ggg cca cct cga tgg gac ccc tat cac ctc			462
Val Lys Ala Ser Ile Pro Gly Pro Pro Arg Trp Asp Pro Tyr His Leu			
90	95	100	
tcc aga gac ctg tac tac ctc act gtg gag tcc tca gag aag gag agc			510
Ser Arg Asp Leu Tyr Tyr Leu Thr Val Glu Ser Ser Glu Lys Glu Ser			
105	110	115	120
tgc agg acc ccc aaa gtg gtt gac atc ccc act tac gag gaa gcc gtg			558
Cys Arg Thr Pro Lys Val Val Asp Ile Pro Thr Tyr Glu Glu Ala Val			
125	130	135	
agc ttc cca gtg gcc gag ggg ccc cca aca cca cct gca tac cct acg			606
Ser Phe Pro Val Ala Glu Gly Pro Pro Thr Pro Pro Ala Tyr Pro Thr			
140	145	150	
gag gaa gcc ctg gag cca agt gga tgc agg gat gcc ctg ctc agc acc			654
Glu Glu Ala Leu Glu Pro Ser Gly Ser Arg Asp Ala Leu Leu Ser Thr			
155	160	165	
cag ccc gcc tgg cct cca ccc agc tat gag agc atc agc ctt gct ctt			702
Gln Pro Ala Trp Pro Pro Pro Ser Tyr Glu Ser Ile Ser Leu Ala Leu			
170	175	180	
gat gcc gtt tct gca gag acg aca ccg agt gcc aca cgc tcc tgc tca			750
Asp Ala Val Ser Ala Glu Thr Thr Pro Ser Ala Thr Arg Ser Cys Ser			
185	190	195	200

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ggc ctg gtt cag act gca cgg gga gga agt taaaggctcc tagcaggctcc 800

Gly Leu Val Gln Thr Ala Arg Gly Gly Ser

205

210

tgaatccaga gacaaaaatg ctgtgccttc tccagagtct tatgcagtgc ctgggacaca 860

gtaggcactc agcaaacggt cgttgttgaa ggctgttcta tttatctatt gctgtataac 920

aaaccacccc agaatttagt ggcttaaaat aaatccatt ttattatgt 969

<210> 148

<211> 1241

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (20)... (517)

<400> 148

atttcggggc ggtaccaag atg gac tcc tcg cgg gcc cga cag cag ctc cgg 52

Met Asp Ser Ser Arg Ala Arg Gln Gln Leu Arg

1

5

10

cgg cga ttc ctc ctc ctg ccg gac gcc gag gcc cag ctg gac cgc gag 100

Arg Arg Phe Leu Leu Leu Pro Asp Ala Glu Ala Gln Leu Asp Arg Glu

15

20

25

ggt gac gcc ggg ccg gaa acc tcc aca gct gtt gag aaa aag gag aaa 148

Gly Asp Ala Gly Pro Glu Thr Ser Thr Ala Val Glu Lys Lys Glu Lys

30

35

40

cct ctt cca aga ctt aat atc cat tct gga ttc tgg att ttg gca tcc 196

302/307

Pro Leu Pro Arg Leu Asn Ile His Ser Gly Phe Trp Ile Leu Ala Ser
 45 50 55
 att gtt gtg acc tat tat gtt gac ttc ttt aaa acc ctt aaa gaa aac 244
 Ile Val Val Thr Tyr Tyr Val Asp Phe Phe Lys Thr Leu Lys Glu Asn
 60 65 70 75
 ttc cac act agc agc tgg ttt ctc tgt ggc agt gcc ttg ttg ctt gtc 292
 Phe His Thr Ser Ser Trp Phe Leu Cys Gly Ser Ala Leu Leu Leu Val
 80 85 90
 agt tta tca att gca ttt tac tgc ata gtc tac ctg gaa tgg tat tgt 340
 Ser Leu Ser Ile Ala Phe Tyr Cys Ile Val Tyr Leu Glu Trp Tyr Cys
 95 100 105
 gga att gga gaa tat gat gtc aag tat cca gcc ttg ata ccc att acc 388
 Gly Ile Gly Glu Tyr Asp Val Lys Tyr Pro Ala Leu Ile Pro Ile Thr
 110 115 120
 act gcc tcc ttt att gca gca gga att tgc ttc aac att gct tta tgg 436
 Thr Ala Ser Phe Ile Ala Ala Gly Ile Cys Phe Asn Ile Ala Leu Trp
 125 130 135
 cat gtg tgg tgc ttt ttc act cca ttg ttg ttg ttt acc cag ttt atg 484
 His Val Trp Ser Phe Phe Thr Pro Leu Leu Leu Phe Thr Gln Phe Met
 140 145 150 155
 ggg gtt gtc atg ttt atc aca ctc ctt gga tgattt ccgaagagac 530
 Gly Val Val Met Phe Ile Thr Leu Leu Gly
 160 165
 aggtcttct atgtgccca ggctgtcttt gaactcctgg gatcaagtga tcctcctgcc 590
 tcagccttcg aagtagttgg gactacaggc ccacgccacc gtgcctggct ggacatgtaa 650

303/307

atttgaagtg aatggttaaa catccagcta gctgaaagca tggcagaccc taacagaaaa 710
 gctacagtgt gtttttgcag ctatgaagtg aatggtttcc tggggaaaat tgtgactttg 770
 tataactgtt gtigaaacca gaataaatta tatttcactt gcatatgcat aaattattaa 830
 aattttcaga agtcagtgat acagaagtac tattttgcaa tgtaaatctg tttgagtctt 890
 tggagaaagt ggtttcattg taggtacata gtgcaactgtt aatattttta acaagtagtt 950
 cactcttcca ttttaaggat agcagttcct tgtataaaat gactggatgt gtataaagga 1010
 attatgttgt catgtgcctt taaccagctt tagtaattac tataatctca ttttatgat 1070
 agttttgtta ggtgacagga ccaaagaaa atattttatg tttctcctc actttagatt 1130
 ttatcattat gtacattact gggtttttag catttcttaa tgtgaagttt taatcacttt 1190
 taagtataca tttttttctg tatcatttaa ataaaatatt tttataactt t 1241

<210> 149

<211> 1174

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (187)... (675)

<400> 149

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 agcaaggga acagctctca ttcaaaggaa ctagaagcct ctccctcagt ggtagggaga 120
 cagccaggag cggttttctg ggaactgttg gatgtgcctt tgggggccc agaaaacaga 180
 aggaag atg ctc cag acc agt aac tac agc ctg gtg ctc tct ctg cag 228

Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln

1

5

10

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ttc ctg ctg ctg tcc tat gac ctc ttt gtc aat tcc ttc tca gaa ctg	276
Phe Leu Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu	
15 20 25 30	
ctc caa aag act cct gtc atc cag ctt gtg ctc ttc atc atc cag gat	324
Leu Gln Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp	
35 40 45	
att gca gtc ctc ttc aac atc atc atc att ttc ctc atg ttc ttc aac	372
Ile Ala Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn	
50 55 60	
acc ttc gtc ttc cag gct ggc ctg gtc aac ctc cta ttc cat aag ttc	420
Thr Phe Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe	
65 70 75	
aaa ggg acc atc atc ctg aca gct gtg tac ttt gcc ctc agc atc tcc	468
Lys Gly Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser	
80 85 90	
ctt cat gtc tgg gtc atg aac tta cgc tgg aaa aac tcc aac agc ttc	516
Leu His Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe	
95 100 105 110	
ata tgg aca gat gga ctt caa atg ctg ttt gta ttc cag aga cta gca	564
Ile Trp Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala	
115 120 125	
gca gtg ttg tac tgc tac ttc tat aaa cgg aca gcc gta aga cta ggc	612
Ala Val Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly	
130 135 140	
gat cct cac ttc tac cag gac tct ttg tgg ctg cgc aag gag ttc atg	660

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Asp Pro His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met

145

150

155

caa gtt cga agg tgacctet tgtcacactg atggatactt ttccttcctg 710

Gln Val Arg Arg

160

atagaagcca catttgctgc tttgcaggga gagggtggccc tatgcatggg caaacagctg 770

gactttccaa ggaagggttca gactagctgt gttcagcatt caagaaggaa gatcctccct 830

cttgacacat tagagtgtcc ccacgggtct ccagtgcggc atcccttctt tgccttctac 890

ctctgttcca ccccttttcc ttccttttct ctctgtacca ttcattctcc ctgaccggcc 950

tttcttgccg aggggttctgt ggctcttacc ctgtgaagc tttccttta gcctgggaca 1010

gaaggacctc ccagccccc aaggatctcc cagtgcacaa aggatgcgaa gaggatagat 1070

tacgtgctcc tgactgatca caccgcagac atttagattt ttatacccaa ggcacttta 1130

aaaaatgttt tataaataga gaataaattg aattcttggt ccat 1174

<210> 150

<211> 1012

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (208)... (873)

<400> 150

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cggcctccca gcgtcccaa gccgcagcgg ccgcgcccct tcagctagct cgctcgtcgc 180

306/307

ctctgcttcc ctgctgccgg ctgcgcc atg gcg ttg gcg ttg gcg gcg ctg 231
 Met Ala Leu Ala Leu Ala Ala Leu
 1 5
 gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag aat 279
 Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln Asn
 10 15 20
 gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct cca 327
 Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro Pro
 25 30 35 40
 cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac aag 375
 Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr Lys
 45 50 55
 gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca aca 423
 Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr Thr
 60 65 70
 ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act atc 471
 Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr Ile
 75 80 85
 cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat ttt 519
 Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp Phe
 90 95 100
 gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg tta 567
 Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met Leu
 105 110 115 120
 act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg tct 615

307/307

Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu Ser
 125 130 135
 ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca gga 663
 Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser Gly
 140 145 150
 ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc acc 711
 Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Thr
 155 160 165
 tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg ttc 759
 Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val Phe
 170 175 180
 ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat gca 807
 Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr Ala
 185 190 195 200
 aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc aga 855
 Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr Arg
 205 210 215
 gtt ctc ttt att tat taaagatggt ttctggcaaa ggccttcctg catttatgaa 910
 Val Leu Phe Ile Tyr
 220
 ttctctctca agaagcaaga gaacacctgc aggaagtgaa tcaagatgca gaacacagag 970
 gaataatcac ctgctttaaa aaaataaagt actgttgaaa ag 1012

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(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS

(57) Abstract: The present invention provides human proteins having hydrophobic domains, DNAs encoding these proteins, expression vectors for these DNAs, transformed eukaryotic cells expressing these DNAs and antibodies directed to these proteins.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/JP 00/05356

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C12N1/21 C12N5/10 C07K14/47 C07K16/18

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

STRAND, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 13074 A (TSURITANI KATSUKI ;YAZAKI MADOKA (JP); MATSUMOTO KAYO (JP); TAISHO) 18 March 1999 (1999-03-18) SEQ ID NO:1 is 100% identical to SEQ ID NO:1 of present application figure 5 -----	1-7

☐ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

27 November 2000

Date of mailing of the international search report

19.02.01

Name and mailing address of the ISA

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Authorized officer

Herrmann, K

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP 00/05356

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1 - 7 (all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: Invention 1: Claims 1-7 (all partially)

Polypeptide comprising an amino acid sequence as in SEQ ID NO:1 and subject-matter relating thereto. Polynucleotides encoding the polypeptide of SEQ ID NO:1 such as a polynucleotide comprising a polynucleotide sequence as in SEQ ID NO:11 (coding sequence) or a polynucleotide consisting of a polynucleotide sequence as in SEQ ID NO: 21 (complete cDNA sequence) and subject-matter relating thereto.

2. Claims: Invention 2-50: Claims 1-7 (all partially)

Idem as subject 1 but limited to each of the polypeptides as in SEQ ID NOs:2-10, 31-40, 61-70, 91-100 and 121-130 and polynucleotides as in SEQ ID NOs:12-20, 41-50, 71-80, 101-110, 131-140 and SEQ ID NOs:22-30, 51-60, 81-90, 111-120 and 141-150, respectively. Invention 2 is limited to subject-matter relating to SEQ ID NOs:2 (protein), 12 (coding sequence) and 22 (complete cDNA), invention 3 to SEQ ID NOs 3, 13 and 23, etc.

Information on patent family members

PCi,JP 00/05356

Form PCT/ISA/210 (patent family annex) (July 1992)



1. The first part of the document is a list of names and addresses. The names are written in a cursive script, and the addresses are written in a more formal, printed style. The list is organized into two columns, with names on the left and addresses on the right. The names are: John Smith, Mary Jones, Robert Brown, and Sarah White. The addresses are: 123 Main Street, New York, NY 10001; 456 Elm Street, New York, NY 10002; 789 Oak Street, New York, NY 10003; and 1010 Pine Street, New York, NY 10004.

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